

1/52

#7  
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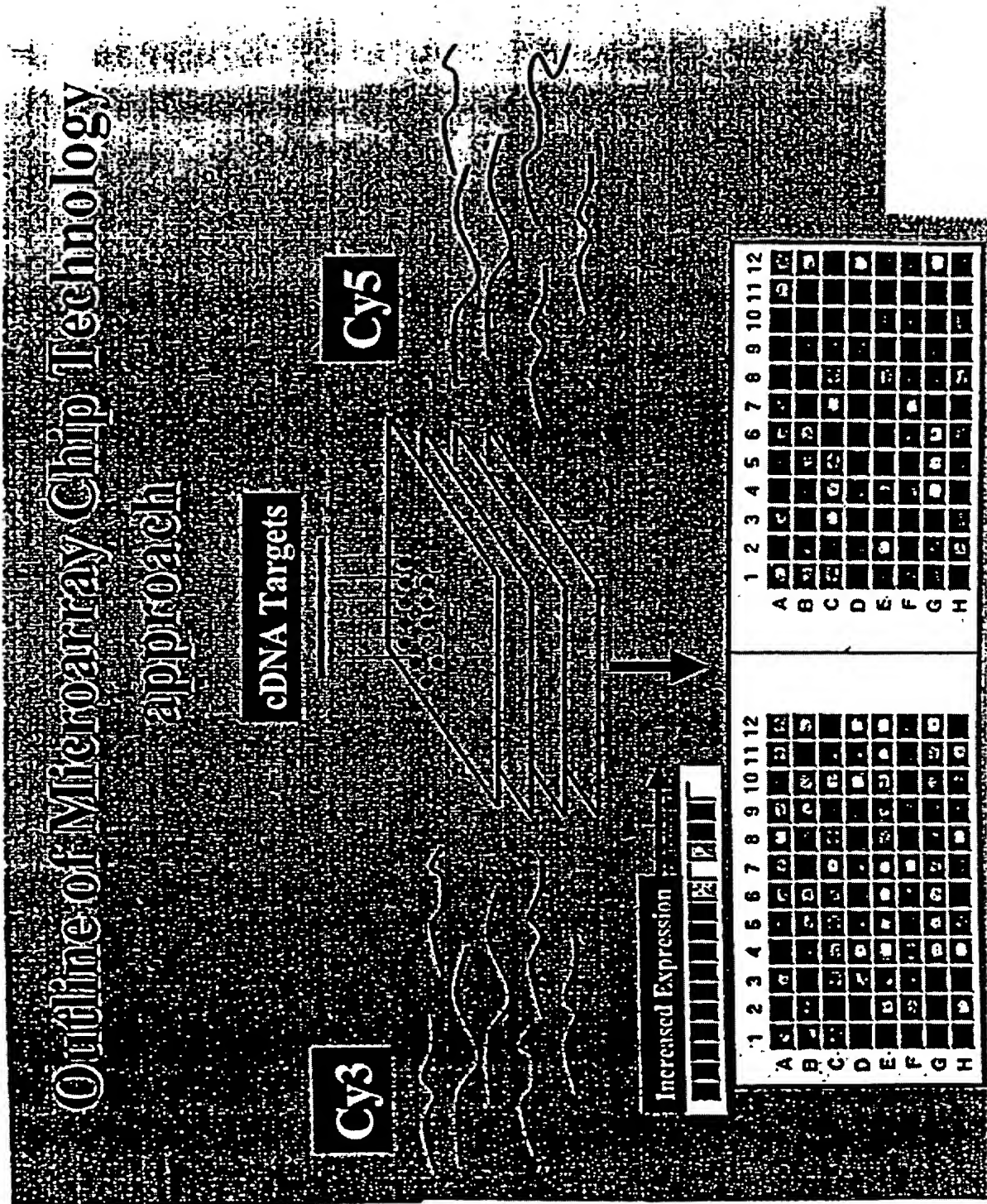


FIG. 1

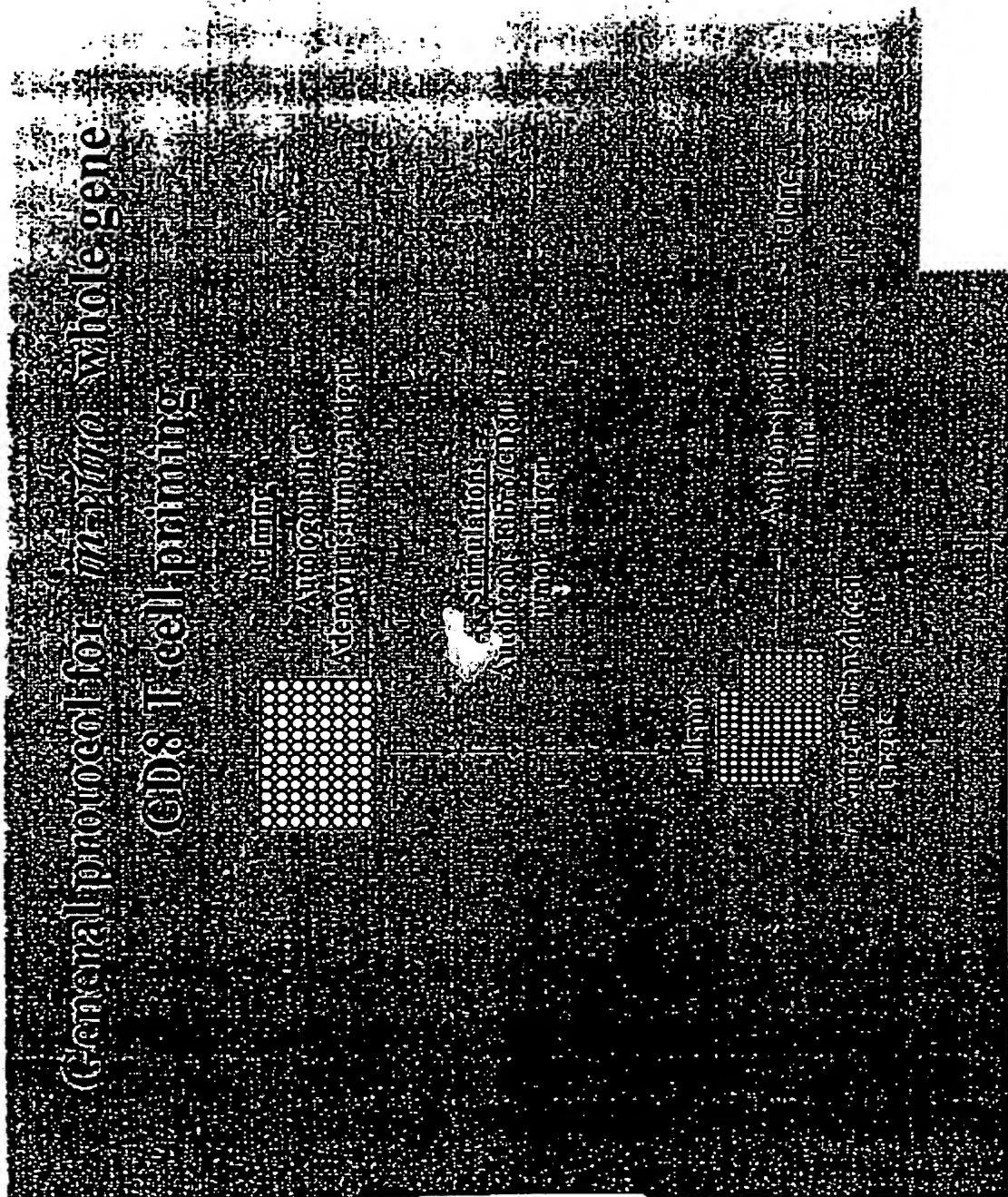
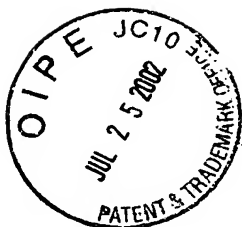


FIG. 2



**LEUKEMIA/LYMPHOMA CHIP #3: PROBES USED IN ANALYSIS**

Cy3 Probe		Cy5 Probe	
Tissue	RNA#	RNA#	Tissue
Lymphoma, T cell	952	SPACT74	Kidney N
Lymphoma, B cell	955	SPACT81	Liver N
Lymphoma, B cell	953	SPACT78	Lung N
Lymphoma	916	SPACT42	Brain N
Lymphoma, Hodgkins	950	138598B	Skin N
Lymphoma, Hodgkins	950	SPACT49	Bone Marrow N
Lymphoma, B cell	CL151	888	PBMC resting
Lymphoma, T cell	904B	SPACT55	Stomach N
Lymphoma, Hodgkins 500 RNA 959	CL153	SPACT70	Thymus N
Lymphoma, B cell	CL152	SPACT75	Skeletal Muscle N
Lymphoma, B cell 500 RNA 958	CL155	SPACT73	Heart N
Lymphoma, B cell	844	243502B	Esophagus N
Lymphoma, B cell	958	1006	Colon N
Lymphoma, B cell	954	SPACT65	Small Intestine N
Lymphoma	960	779B	Trachea N
Lymphoma, T cell	957	S9327328	Bladder N
Lymphoma, B cell	914B		
Lymphoma, B cell	913		
Lymphoma, B cell	944B		
Lymphoma, B cell/failed	903		

GREEN: Tumor probes where gene expression would be desired.  
 RED: Normal essential tissue probes where gene expression is to be avoided.  
 BLACK : Normal tissue probes where gene expression is acceptable.

[illegible]

**FIG. 5**



High Differential Expression in Group 1      All Mean Signal 1 > 0.3  
All Lymphomas > N comparison for Lymphomas  
Threshold : 3

Seq. Element (BP) BP Ratio Signal 1 Signal 2										Gene Chrom Contig Contig Gene Chrom									
ID No. a,1																			
10,548	R0410 D9	389	40.12	0.307	0.008	0	0	21 (0704289)	3	0	3	0	2	1					
10,532	R0411 D1	274	37.21	0.406	0.011	1	5262708	mRNA, cDNA DNF265661123	57 (13205739)	1	0	1	2						
10,514	R0442 H5	262	16.37	0.304	0.022	12	13642667	poly(A)-binding protein, cytoplasmic 1 (PABPC1)	18 (0603377)	0	0	2	0						
10,555	R0413 B9	509	13.46	0.369	0.027	0	0	37 (10309002)	1	0	1	1							
10,547	R0412 A1	332	12.1	0.455	0.036	7	8506072	hypothetical protein (FLJ20323), mRNA	90 (4775342)	1	0	1	1						
10,561	R0410 C5	729	9.87	0.554	0.067	2	12394450	DNA seq. from clone RP11-20716 on Chr. 13	46 (11500033)	5	0	3	4						
10,572	R0441 B1	582	8.79	0.873	0.009	176	5970606	Gaonic, chromosome 6p21.3, HLA Class I region	34 (7066360)	0	0	0	2						
10,553	R0412 C9	363	8.33	0.341	0.051	7	0	0	150 (12003092)	1	0	1	0						
10,541	R0408 E10	919	5.25	0.332	0.062	0	11630464	gene FLJ20675 PRO2870 mRNA	1 (7113300)	1	0	1	0						
10,562	R0409 B1	364	4.55	0.214	0.071	1	13000431	12 BAC RP11-61298	14 (10289152)	2	0	2	1	0					
10,569	R0439 B4	471	4.4	0.26	0.062	12	12633014	protease (serpin, macropain) subunit, beta type	29 (1280506)	1	0	2	2						
10,551	R0410 G11	530	3.44	0.218	0.095	3	3237053	mRNA for KIAA005 protein, partial cds	29 (1280506)	1	0	2	2						
6.1-6.3																			
10,576	R0437 A6	231	10.18	1.761	0.172	22	219402	endoplasmic reticulum factor 4A1	4 (12674065)	3	0	2	1						
10,567	R0438 F6	465	7.75	0.193	0.193	33	13270605	RAK, member RAS oncogene family	1 (12309009)	1	0	1	0						
10,565	R0438 C4	653	6.12	1.053	0.14	41	65666005	MLF2 suppressor (HSM17)	4 (5304077)	0	0	4	0						
10,580	R0469 F1	653	6.82	1.03	0.151	25	184231	non-histone chromosomal protein H4C-14 gene	80 (7352544)	3	0	0	4						
10,545	R0410 A7	375	6.5	0.569	0.146	0	0	0	22 (1155912)	10	1	6	1						
10,540	R0408 D1	233	4.97	0.812	0.173	7	12803586	hypothetical protein FLJ20647, clone MGC3443	10 (13128911)	1	0	1	0						
10,550	R0408 D9	522	4.17	0.766	0.164	25	4590326	proteasome activator subunit 2 (PACT2 gene) (PACT2)	146 (14607263)	14	0	5	5						
10,577	R0437 B7	433	3.87	0.47	0.110	4	15546577	hypothetical protein DNF265640632	0	4	0	2	3						
10,556	R0418 A2	534	3.91	0.429	0.108	6	10440178	cDNA, FLJ23478 fa, clone HSI14935	39 (12428993)	3	0	2	3						
10,550	R0410 F10	208	3.9	0.435	0.112	1	5100307	genomic DNA, Chr. 22q11.2, clone NG1265D1	4 (2306224)	0	0	1	0						
10,543	R0409 B7	327	3.87	0.509	0.131	1	4500154	mRNA, cDNA DNF26566A0510	80 (12710843)	3	0	3	3						
10,557	R0418 D12	546	3.85	0.416	0.106	0	1047062	mRNA, cDNA DNF26566A0510	80 (12710843)	13	0	0	0						
10,544	R0409 D12	542	3.71	0.569	0.153	1	14329055	cDNA, FLJ21562 fa, clone CCL08450	126 (12800019)	9	0	2	5						
10,579	R0439 D2	342	3.66	0.513	0.14	1	6907710	chromosome 5 gene CTC-647M3	126 (12800019)	9	0	0	8						
10,563	R0438 C1	377	3.56	0.418	0.117	2	2338184	cDNA DNF26566C1114	83 (1287237)	9	0	0	2						
10,549	R0419 E1	356	3.46	0.347	0.1	0	10436346	regulator of G protein signaling (RGS13)	35 (2910346)	4	0	2	1						
10,559	R0417 E7	354	3.44	0.35	0.102	3	0	0	117 (12323253)	6	0	6	2						
10,554	R0413 A5	364	3.4	0.246	0.102	0	0	0	19 (1159096)	8	0	4	0						
10,539	R0407 B1	369	3.29	0.414	0.136	0	0	0	22 (2042706)	2	0	3	1						
10,538	R0407 D4	378	3.17	0.321	0.101	2	6102660	mRNA, cDNA DNF26566P171 (clone DNF26566P171)	59 (11681430)	1	0	0	1						
10,566	R0407 F4	180	3.15	0.418	0.132	8	13033789	hypoxanthine carbanion-ase, antigen 66 (HCA66)	1 (12156867)	1	0	1	1						
10,537	R0408 H9	693	3	0.321	0.107	3	2981098	chase 23765 mRNA seq.	32 (1137727)	1	0	1	0						
6.2																			
10,568	R0439 C11	678	13.02	3.704	0.265	51	14126543	Proteomic protein L4	7 (2306441)	1	0	1	2						
10,546	R0419 B6	408	10.85	4.045	0.36	1	10105402	DNA seq. from clone RP11-433182 on Chr. 13	38 (107131492)	5	0	0	5						
10,564	R0438 C10	467	7.79	1.56	0.25	45	14141113	high-mobility group (pentamerous domain) protein (HMG22)	239 (14053454)	8	0	5	5						
10,570	R0440 E11	411	6.33	2.361	0.380	135	13438316	nuclein alpha 5	14 (112771100)	8	0	9	1						
10,578	R0458 C7	430	5.36	3.701	0.69	0	0	0	101				100						
10,573	R0441 B6	339	4.09	0.305	0.221	44	5566606	MLF2 suppressor (HSM17)	3 (5434300)	8	0	3	2						
10,542	R0409 A5	568	3.69	0.757	0.205	1	7022880	cDNA FLJ10754 fa, clone NT878304544	31 (9807449)	2	0	0	3						
10,558	R0417 C3	498	3.27	1.776	0.543	10	6610780	cDNA DNF26566O1224 (from clone DNF26566O1224)	66 (123017211)	11	0	7	0						
10,575	R0445 D10	305	3.26	1.965	0.607	42	13033568	nucleic acid sensitive element binding protein 1 (NLSBP1)	115 (112786428)	11	0	0	9						
10,571	R0440 H9	303	3.21	0.616	0.254	0	0	0	45 (2400028)	3	0	3	0						

**FIG. 6**

# Hematology therapeutic Ab candidates

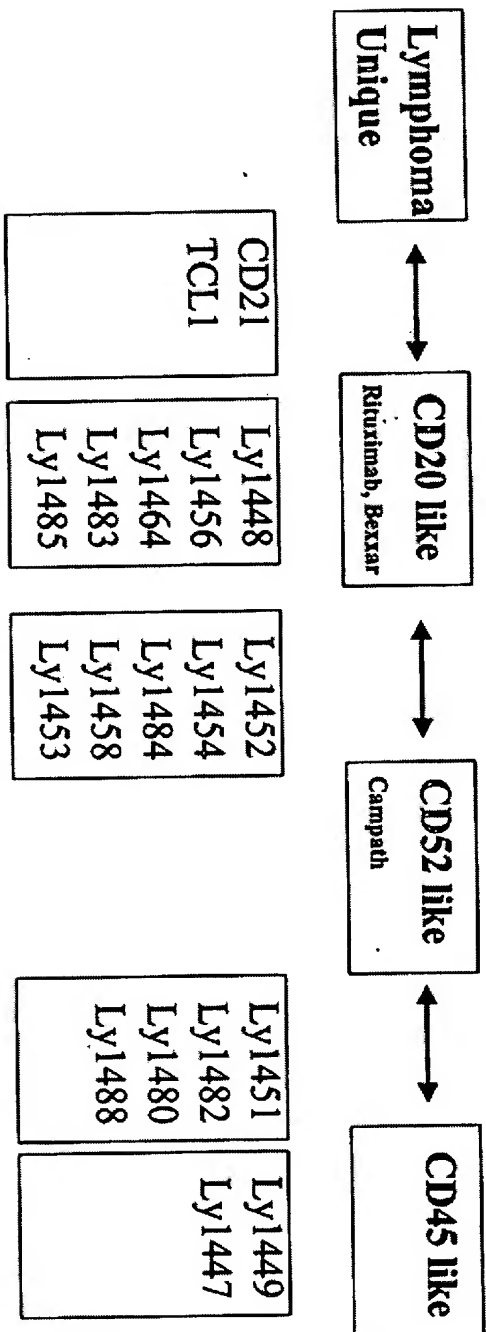
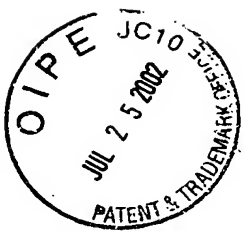


FIG. 7

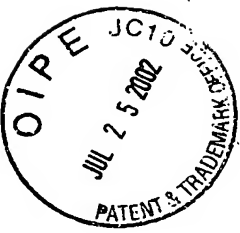


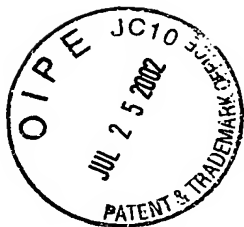
# Identification of lineage specific markers and candidate lymphoma, leukemia and myeloma antigens

Gene	CD34+	CD19+	CD14+	CD2+	Ly	Hodgkin	Myeloma	CLL <sup>+</sup>	AML
CD20	-	+++	-	-	+++	+	+	++	+/-
CD21	-	+	-	-	+++	++	+	+	-
TCL1	-	+	-	-	+++	+	-	++	-
LY1448	-	+++	-	-	+++	+	++	++	-
LY1452	-	+++	-	-	+++	+	+	++++	+/-
LY1456	-	++	-	+	++ T-NHL	+	++	++++	-
LY1464	-	+++	-	-	+++	+	n.d.	n.d.	n.d.
LY1483	-	+++	-	+	+++	++	+	n.d.	-
LY1458	-	+++	-	+	+++	+	n.d.	n.d.	n.d.
LY1481P	-	+++	-	+	+++	+	n.d.	n.d.	n.d.
LY1485P	-	+++	-	-	++	-	n.d.	n.d.	n.d.
LY1480	+	++	++	+	+++	+	n.d.	n.d.	n.d.
LY1488	+	++	++	+	+++	+	n.d.	n.d.	n.d.
LY1484	+	++	+/-	+/-	+++	++	n.d.	n.d.	n.d.
LY1482	++	+++	++	+++	+++	++	n.d.	n.d.	n.d.
LY1453	++	++	++	++	+++ T-NHL	+++	+++	+++	+++
LY1449	++	+	-	-	+	+	+	+++	++
LY1447	++	+++	+	+	++	++	n.d.	n.d.	n.d.
LY1451	++	++	-	-	++	+	+	++	++++
CD52	++	+++	++	++	++	++	n.d.	++	n.d.
CD45	+++	+++	+++	+++	+++		n.d.	n.d.	n.d.

\* single probe

Figure 8





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SEQ ID NO:

10,581

Lyl447 sequence:

CCCTCAACAGACTGGATGGGGTCCACCCACATTAGGCTGGAGTTTGTTCGCACTGTGCAGTTATCATTCTGGGATGGG  
GGTACCTTACTCTCCCAATGAGAAATTTCTAAATTTCTCTTTTGAAGCTGGTGGCTCCACCTTCTCANAACTGCATAGGG  
CGTGAGCTTTGTGTGGTATGTGACCTCCAGAAACAGACTGTGAGCAGATTTTTCTTTAATCTGAGCCTATGCTTGCTG  
CTGTCCTTCTTGACTTCAACTAGGCTTAAAAAGCGN

SEQ ID NO:

10,582

Lyl448 Sequence

CCAGGGTTAGGACATTCAAATGTCTTTATCCACATTCTGAAAGGATAATTGTTATAGATTCCCTACCTCCATAGGAATGC  
TTATAATGGATTATCTATACAACTCCACATTCCACATTTTGCAATAGAGATGGAATCAGTCAAACCTGTGCCAGA  
GTTTCCCTTAGAGTTCTCACCTGTGTCTTTATATCCATCTAGGAATCCCATCTCTAATGTAAGCTTGGAGATCCGGGCC  
CCCGGGGACAGGTGACTGAAGGACAAAACCTGATCTGCTCTGCTCAGTGGCTGGGGGTACAGAAATGTCACTTCTC  
CTGGTACAGAGAGGCCACAGGAACCACTATGGGAAAGAAACCCAGCGTTCCCTGTGACAGAGCTGGAGATCCAGCTG  
TGAAGAGAGTGTGCGGCAAAATATTACTGTAGAGCTGACAACGGCCATGTGCTATCCAGAGCAAGGTGGTGAATATC  
CCTGTGAGAGACCTGATGGCTATAGAAGAGACCTCATGACAG

SEQ ID NO:

10,583

Lyl449 Sequence

CCACATTGGGAATTTGTCACACAGGTGCTGCTCCACCAACAGAGAGGCTCAGGAGATTGTCCAGGGACAAGGAGACCT  
GGCCGGACCTCTGACAGGAGGTGAGGGCCCTGCCCCATCTTGTCCCATCACATTCTGGATGTTGGCATCCOCAGGCTC  
CTGGGAGGGGAGAGTGTGATAAAAGGCCAAAAATCACACAGAAAGAGACAGAAAACTCCACGCACTTCTACATAG  
GTGCTACCGTATTCTACGAGCACGGGGCTGTGTTGAAGACTCCCTCTGGAAGTTACAGAAAGGAGCCACAGAGGTTT  
AGCCTCACGCTCTTCTCAGATGCAGTCAACACTTTACCAAACTTGGCACATCCAACTCTTTTCAATATTTTACA  
CCTGTTGTGGCTGCTGACAGATATTTGTNATTGATCTTTCTAATTTACGGGATTCTAAATGTGTTTGTAGAATCTG  
GTCAGCACTCAAGGATTCTGTCTTT

SEQ ID NO:

10,584

Lyl451 Sequence

CTGCTGCTAAATACCTMTGAGAACTCTGCTTCTATCTAAGGGGACCTACTTTTNTCNGGAATCTCAATACTTGGAAACAA  
GAACCTCTTANACGGACCTTTGGCATATGAATTTGGACCACTGTAGGTTCCAGGACTAGAGAGCCAGCAATGCCTCCA  
TGAACAACTCACCAATTACTCTGCTCAGGAAACGAGGTAACTGTAGACAGCCGAGGCCCTTAGGGCGGCTTAGG

SEQ ID NO:

10,585

Lyl452 Sequence

AAANACCAATAGCAGCCAAAACAGAACTTTGTAAACAAAACCACTATCAGCCCTGTGCTTAAACACAGAACTGCG  
ATTCTTTTGAACATTAAGTATATGCAATAAGAGAAATAGAACATCTTTTCTTAAATATACAAATACCAATATCTAA  
AACAAATGTCACCAATAATAGACACAAATCGGTGTTATCATAGGCACTGTGAACAGTCTTTTTCACAGTACTCAGGGCA  
TCATGGGGCTGACAGGGCCACACTTTCCAGAAATTTTCTCTGCTGTGATCCTGCGCACCCCGGGGCACTCGGAGGACT  
GGAAGCACTGTTTGTAAAGCAAGCCCTGCAAGCTGAACATCTTCTACATGTTGCTGTCTGAAATGGGAGATGACAGTC  
GTATTCTGGCAAAATTCACAAATAAGCCCTTTCTCTGACACAGCTCACAGCCAGCCACATGTGCAAGGGAAGCTTGNAG  
AATGTCCTTGAGTAAGGGTGCAGCAGCCCTTTCTTGATCTGACCAAGTCTCAAGGGAGAACAGGTGGAGCTCATCAG  
TCAAGTGTCCCGCCCTGCCCTACAACTCTTTAATGCACTGTTAGCAAACTACAGGTCTTCAACAGCTTCTTGATAT  
GGAAGAGCTGCTCTGAATTTCTCTC

SEQ ID NO:

10,586

Lyl453 Sequence

CCAAAACTTCAGCATAAAACTATCCTGCTGTGTATTATATATATTTATTACNNNATTTAATAACAAAAACCACTTT  
TGAACCAAGTAATTTTATCTAGTGTGAAAGAAATTAATCACATGGTCTATATACTGGCTAGTGTCTCTTAAAAGTAGACA  
TTAAATATTTTCAATTTGAGGGAATCTTTGGAGATTAGTGGCATCTAATCTTGGGGCTCAGACACCCAAATCTATA  
TATTGACAGTGAAGTTGATGATTGTTATCAAAATTTCAAGCACTAATGGAAACCCCACTTCTCTGTGAAGATT  
TTCACTGCTTTACAGTTATTGAAATTTTCAATTTCTGTGAGGCCACTTCAGAACTCCCAATGGGCTTTGCAATATT  
AAATGTGGAGAAATGCATTAATCATTATTTAATCAATGAGTTT

SEQ ID NO:

10,587

Lyl454 Sequence

CCTCTCCACAGGCTGCTTGAGTGTCTCATGACACAACAGTTGGCTTACTCCAGAGTGAGCAACTCAAGAGAGAGCAAGG  
CAGAAGCTACCAATCTTTATGTTTGAAGTCATGCACCACTCTTTTCAAGAGTATCCTGTTGATTATTTGATCAGCTTG  
TTCACTGTGGAGGGAATTCACAAGGGCATGAATACTCCACTGGCAAGGATCATTTGGGGCCATCTTGGAAAGCTGTGTG  
AATGAGCAATGAATGCACAGATAGAATATTAGCAGTGCAATGATGCTAGAGGTCACTACCCCACTGTCTCTGTGCTC  
TTCTCCCCAACCCCTCCCTGCTCCAGGCAAGAGCCCTTAGCCTCTGCTTGATCACTTTCAAGCACTCAACATCTTCA  
GGAAACCTATTCCGCGTGGGACAGTGTAAATTAGTGGAAACTCTTTTCAAAAGTTGAATCAGTTCTCTGTGTCTTA  
TTACCTGCTGATCACTGTCCAGACTCTGAGGACACAGAGCAAGTTTATTCTCTTACTGATGTTAGCTTTTCAAGTATC  
CATCCCTTCCCTCAGTATATTAGAGTTACGTAATTTCTAAATGCTTAGCAGCTCATTATCCTGAACA

SEQ ID NO:

10,588

Lyl456 Sequence

AAAGACATGAAAAATATCCCAAGATCATACTAGATCATAATAGCAATTCCTTTACAAATGAATTTAGAGGTAAGTATC  
TCTAACAGTTTCTTTCATGTTGTTTAAATGCAAGGGCCAGAGGATCTGCCAGCCCTTGGAAACAGCGTGAGCTAACCCAC  
GTGCTATAGACACTTCATGTTGCTTACCCAGGGAGTCAAGCGCTTTGCTCCCTCACTGTCTGTGAGTCTCAGGCCATC  
TAGTAGCCACCCCGCTGCTCCAAACTTGAAGTTGTTTCAAAATGTTTCTCACTGTTTCACTCTCTCACTGACCCCACTC  
CAGAAAGCTGGAGAGAGGCCAAGATGCCACCCACTTCCCAATCCCTCGCCACAGATCTGTGTCTATCACACACTCTG  
TAAAGTGCCTGCTTCTCTCTCTTGAAGAGCTGAGAACACACATTTAATGTTTAAAGAAATGGGGCAGGCTAA  
AAATGACTGATCCCAAGCGGCTGACTCA

SEQ ID NO:

10,589

Lyl458 Sequence

TTGAATGCTCTATTTTGCNNNTAANNNTTATTNACTAGTCTCAGTAATACATTAGTAAAAANCATGTGNTTAAATTAAT  
GGGTTANAATCAANAACATANAAGTGGGCAATATACCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT  
ATTCCTCAATATTTTGGGAAACATNANAANATGGGTTGCTTGAAGTAANANATTAANAANAATTAAGCTTTTGTATCCCTG  
CCAAACACCCATGCCAGGGGGGNCACCTTCAATCAATAACATGCCAGGAANAGTAAGNTGCCCTTCTGANGCCGNA  
ATCTGCCATCATNTTCCATNTTCCAGCTNTTCCATTTGTCNAGNCAATCTGGGCTCTCAGGATNATACCCGGTCTTA



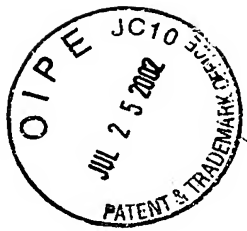
Figure 1a. Lyl464 full length DNA sequence (SEQ ID NO: 10,597)

1	gatgcaagga	gatgagacag	ttaaatttac	ttcctctttt	ctaattctgag	aggtttcatg
61	ttgagaataa	tcaagtgttg	gggtgcagca	gccataaaca	cagtcaccat	gaagctgggc
121	tgtgtctcca	tggcctgggc	cctctacctt	taccttgggt	tgctctgggt	ggccgacatg
181	ctactggctg	ccagttttga	gacgctgcag	tgtgagggac	ctgtctgcac	tgaggagagc
241	agctgccaca	cggaggatga	cttacttgat	gcaaggggaag	ctgggttcca	gggtcaaggc
301	tacactttca	ctgaaccctt	ccacctgatt	tgttccctat	actggctgat	cctccaaggt
361	ccagccaagc	cagtttttga	aggggacctg	ctggttctgc	gctgccaggc	ctggcaaga
421	ttggcactga	ctcaggtgac	cttctaccga	gatggctcag	ctctgggttc	ccccgggctc
481	aacagggaat	tctccatcac	cgtgttaca	aaggcgacaga	gcgggcatac	ccacttgcagt
541	ggcatcttcc	agagccctgg	tccctgggatc	ccagaaacag	catctgttgt	ggctatcaca
601	gtccaagaac	tgtttccagc	gccaatcttc	agagctgtcc	ctccagctga	acccaagaca
661	ggaagcccca	tgaccttgag	ttgtcacaga	aaagtgtccc	tgcagaggtc	agctgccccg
721	ctcctcttct	ccttctacaa	ggatggaagg	atagtgcaaa	gcagggggct	ctcctcagaa
781	ttccagatcc	ccacagcttc	agaagatcac	ctcgggtcat	actgggtgtg	ggcagccact
841	gaggacaacc	aagtittgaa	acagagcccc	cagctagaga	tcagagtgtg	gggtgcttcc
901	agctctgctg	cacctcccac	attgaatcca	gctcctcaga	aatcagctgc	tccaggaact
961	gctcctgagg	agggcccttg	gcctctgcct	ccgcgcgcaa	ccccacttct	tgaggatcca
1021	ggcttttctt	ctcctctggg	gatgacagat	cctcatctgt	ataccagatg	gggcttctct
1081	ctcaaacaca	tgcaggatgt	gagagtcctc	ctcggtcacc	tgtctatgga	gttgagggaa
1141	ttatctggcc	accggaagcc	tggggacaca	aaaggtcactg	ctgaatagaa	gtaaacagtt
1201	catcatgatg	ctcaactaac	caccccaata	aatctgattc	tttatcttct	cttctgttcc
1261	tgcacatatg	cataagtact	tttacaagtt	gtcccagtgt	tttgttagaa	taatgtagtt
1321	aggtgagttg	aaataaaatt	atataaaagt	agaattagag	tttagctata	attgtgtatt
1381	ctctcttaac	acaacagatt	ctctgtctct	agatcaggaa	tttctatctg	ttatatcgac
1441	cagaatgttg	tgatttaaa	agaactaatg	gaagtggatt	gaatacacga	gtctcaactg
1501	ggggccaatt	tggcccccag	aggacatttg	gcaattgttg	gagacatttt	gggtcattata
1561	cttgggggggt	tgggggatgg	tgggattgtg	gtgctactgg	catccagtaa	atagaagcca
1621	ggggtgccgc	taaacaatct	ataatgcaca	gggcagttac	ccacaacgaa	aaataaatctg
1681	gcccacaaat	tcagttgtac	tgagtttgag	aaaccccagc	ctaatgaaac	cctaggtgtt
1741	gggctctgga	atgggacttt	gtcccctcta	attattatct	ctttccagcc	tcaatcagct
1801	attcttactg	acataccagt	ctttagctgg	tgtatggtc	tgttctttag	ttctagttgt
1861	tatccccctg	aaagccatta	tgttgaactc	ctaatacccc	aggtgatggc	attaagaagt
1921	gggctcttgg	gaagtgatta	gttcaggagt	gcagagccct	catgattagg	attagtgccc
1981	ttatttaaaa	aggccccaga	gagctaacct	accctttccac	catatgagga	cgtggcaaga
2041	agatgacatg	tatgagaacc	aaaaaacacg	tgtcgccaaa	caccgactct	gtcgttgctc
2101	tgtacttgaa	cttccagctc	ccagaactat	gagaaaataa	attctgttgt	ttgt

Figure 1b. Lyl464 protein sequence (SEQ ID NO: 10,578)

MKLIGCVLMAWALYLSLGLVHVAOMLLAASFETLQCEGFPVCTEESSCHTEDDLTDAREAGFQVKAYTTFSEPHLTVSYDWLILQGPAPKV  
 FEGDLLVLRCAQWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVP  
 SAEPQAGSPMTLSCTKLPLQRSAAARLLFSFYKDRIVQSRGLSSEFQIPTASEDHSGSYWCEATEDNQVWKQSPQLEIRVQGASSA  
 APTPLNPAQKSAAPGTAPEAPGLPPPTPSSSDPGFSSPLGMPDPHLYHQWGLLLKHMQDVRVLLGHLLMELRELSGHRKPGTTKA  
 TAE





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## TMpred Report for Ly1464

Date:

SEQ ID NO: 10,598

MKLGCVLMAWALYLSLGVLVVAQMLLAASFETLQCEGPVCTEESSCHTED  
DLTDAREAGFQVKAYTFSEPFHLIVSYDWLILQGPAPVFEGLLVLRQC  
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GPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQR  
SAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVW  
KQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPTPS  
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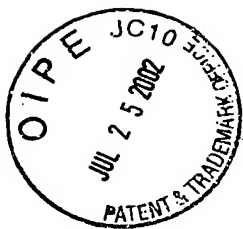
Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1464 has 358 amino acids and 3 Transmembrane Domains

Transmembrane Domain 1: 3 - 24      Score: 1.5484

Transmembrane Domain 2: 71 - 92      Score: 1.3009

Transmembrane Domain 3: 158 - 179      Score: 1.3027



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**Ly 1464 MHC class binding peptides (SERIDNDs: 10,599-10,819)****Ly1464 A1 binding peptides**

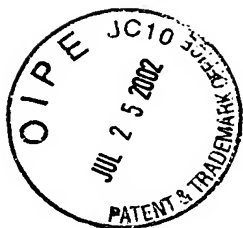
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ATEDNQVWK	243	90
2	ASEDHSGSY	230	67.5
3	FSEPFHLIV	67	67.5
4	LTDAREAGF	52	25
5	SSDDPGFSS	300	6.75
6	ELFPAPILR	167	5
7	SSEFOIPTA	222	2.7
8	MPDPHLYHQ	312	2.5
9	LMELRELSG	339	2.25
10	HTEDDLTDA	47	2.25
11	CTEESCHT	40	2.25
12	ALGPFGFNR	118	2
13	LGMDDPHLY	310	1.25
14	CVLMAWALY	5	1
15	KADSGHYHC	135	1
16	LRELSGHRK	342	0.9
17	QLEIRVQGA	255	0.9
18	WCEAATEDN	239	0.9
19	SAEPQAGSP	179	0.9
20	AREAGFQVK	55	0.9

**Ly1464 HLA A2 binding peptides**

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	YLSLGVLVV	13	4047
2	LLLKHMODV	323	1006
3	VLMAWALYL	6	739
4	VLWVAQMLL	18	301.4
5	MLLAASFET	24	271.9
6	ILQGPAKPV	81	118.2
7	LLGHLLMEL	334	83.53
8	LLAASFETL	25	33.81
9	WQDWPLTOV	102	29.84
10	YTFSEPFHL	65	29.29
11	LIVSYDWLI	73	18.29
12	KLPLQRSAA	195	17.39
13	WALYLSLGV	10	16.44
14	CQAWQDWPL	99	16.24
15	GIPETASVV	153	16.08
16	QVWKQSPQL	248	15.51
17	ALYLSLGVL	11	8.38
18	QMGLLLKHM	320	8.252
19	VVAITVQEL	160	7.309
20	GVLWVAQML	17	6.916

**Ly1464 A3 binding peptides**

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	WLILQFPAK	79	30
2	ELFPAPILR	167	18
3	ALGPFGFNR	118	9
4	VLWVAQMLL	18	6
5	VLMAWALYL	6	5.4
6	LLKHMODVR	324	4
7	KLGCVLMAW	2	2.7
8	PMTLSCQTK	187	2
9	LLGHLLMEL	334	1.8
10	GMPDPHLYH	311	1.8
11	PLTQVTFYR	106	1.8
12	LLAASFETL	25	1.8
13	HLYHQMGLL	316	1.35



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14	ALYLSLGVL	11	1.35
15	YLSLGVLWV	13	1.2
16	ATEDNQVWK	243	1
17	HMQDVRVLL	327	0.9
18	HLIVSYDWL	72	0.9
19	KATTFSEPF	63	0.9
20	KQSPQLEIR	251	0.81

Lyl464 A11 binding peptides

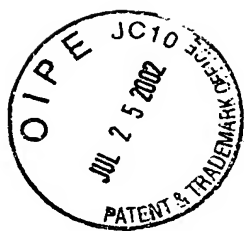
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ATEDNQVWK	243	1
2	WLILQGPVK	79	0.6
3	KQSPQLEIR	251	0.36
4	CQTKLPLQR	192	0.24
5	RVLLGHLLM	332	0.18
6	PTLNPAPQK	270	0.15
7	ELFPAPILR	167	0.096
8	ARLLFSFYK	203	0.09
9	GVLWVAQML	17	0.09
10	LLQHMQDVR	324	0.08
11	ALGPPGPNR	118	0.08
12	GHRKPGITK	347	0.06
13	RVQGASSSA	259	0.06
14	LPLQRSAAR	196	0.06
15	BFSITVVQK	127	0.06
16	YTFSEPFHL	65	0.06
17	ITVQELFPA	163	0.045
18	YHQMGLLLK	318	0.04
19	QVWKQSPQL	248	0.04
20	LFSFYKQGR	206	0.04

Lyl464 A24 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LYHQMGLLL	317	200
2	VFEGLDLVL	89	30
3	TFYRDGSAL	111	20
4	GFQVKAYTF	59	15
5	KPVFEGLDL	87	12
6	HMQDVRVLL	327	10.08
7	GVLWVAQML	17	10.08
8	LYLSLGVLW	12	9
9	IFQSPGPGI	146	7.5
10	APREAPGPI	285	7.2
11	TFSEPFHLI	66	7.2
12	HLLMELREL	337	6.6
13	MTLSCQTKL	188	6.6
14	VLMANALYL	6	6
15	HLIVSYDWL	72	6
16	GCVLMAWAL	4	6
17	LLGHLLMEL	334	5.28
18	VVAITVQEL	160	5.28
19	MAWALYLSL	8	4.8
20	DVRVLLGHL	330	4.8

Lyl464 A68 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ELFPAPILR	167	45
2	ATEDNQVWK	243	30
3	ELRELSCHR	341	22.5
4	DVRVLLGHL	330	18
5	ALGPPGPNR	118	15
6	LPLQRSAAR	196	10
7	ETLQCEGPV	31	9
8	RVLLGHLLM	332	8
9	VVAITVQEL	160	8
10	VVAQMLLAA	20	8



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11	GVLWVAQML	17	8
12	KQSPQLEIR	251	7.5
13	PTLNPAPOK	270	6
14	AVPSAEPQA	176	6
15	ETASVVAIT	156	6
16	VVQKADSGH	132	6
17	WLILQGPAA	79	6
18	LLKHMDDVR	324	5
19	CQTKLPLOK	192	5
20	RVQGAASSA	259	4

Lyl464 B7 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	DVRVLLGHL	330	200
2	KPVFEGDLL	87	80
3	APPEAPGPL	285	72
4	LQSAARLL	198	40
5	QVWKQSPQL	248	20
6	VVAITVQEL	160	20
7	IVSYDWLIL	74	20
8	GVLWVAQML	17	20
9	VLMAWALYL	6	12
10	MAWALYLSL	8	12
11	ALYLSLGLV	11	12
12	HMDDVRVLL	327	6
13	APGTAPEEA	281	6
14	SPMTLSCQT	186	6
15	DAREAGFOV	54	6
16	RVLLGHLIM	332	5
17	HLLMELREL	337	4
18	LLGHLLMBL	334	4
19	VLWVAQMLL	18	4
20	HLVHQMGLL	316	4

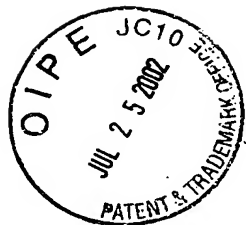
Lyl464 B8 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	DVRVLLGHL	330	8
2	DAREAGFOV	54	7.2
3	LQSAARLL	198	1.2
4	PSFYKDGRI	207	1
5	GCVLMAWAL	4	0.8
6	MAWALYLSL	8	0.8
7	LLGHLLMBL	334	0.4
8	HLVHQMGLL	316	0.4
9	VLMAWALYL	6	0.4
10	AARLLFSFY	202	0.4
11	APILRAVPS	171	0.4
12	ALYLSLGLV	11	0.4
13	HLIVSYDWL	72	0.4
14	LLAASFETL	25	0.4
15	VLWVAQMLL	18	0.4
16	HMDDVRVLL	327	0.3
17	APPEAPGPL	285	0.24
18	LSGHRKPGT	345	0.2
19	GVLWVAQML	17	0.2
20	SSSAAPPTL	264	0.2

Lyl464 B27 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LRELSGHRK	342	2000
2	VRVLLGHLL	331	2000
3	ARLLFSFYK	203	2000
4	AREAGFOVK	55	2000
5	QSAARLLF	199	1000

FIG. 12  
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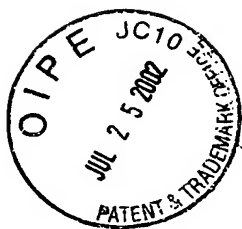
6	GRIVQSRGL	213	600
7	NREFSITVV	125	600
8	KQSPQLEIR	251	300
9	HRKPGTTKA	348	200
10	IRVQGASSS	258	200
11	COAWQDWPL	99	200
12	LRCQAWQDW	97	200
13	HLYHQMGLL	316	150
14	ALVLSLGLV	11	150
15	VLWVAQMLL	18	150
16	CQTKLPLQR	192	100
17	VQKADSGHY	133	100
18	LQGPAPKPVF	82	100
19	AQMLLAASF	22	100
20	KAYTFSEPF	63	75

Lyl464 B35 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KPVFEGDLL	87	60
2	WPLTQVTFY	105	40
3	EPFHLIVSY	69	40
4	TPSSEDPGF	298	30
5	GPPGPNREF	120	20
6	AARLLFSFY	202	18
7	QSRGLSSEF	217	15
8	APPEAPGPL	285	12
9	VQKADSGHY	133	9
10	ASEDHSGSY	230	6
11	KAYTFSEPF	63	6
12	EAGFQVKAY	57	6
13	SSSAAPPTL	264	5
14	LSCQTKLPL	190	5
15	SSCHTEDDL	44	5
16	AATEDNQVW	242	4.5
17	KPGTTKATA	350	4
18	RVLLGHLLM	332	4
19	FPAPILRAV	169	4
20	DAREAGFQV	54	3.6

Lyl464 B44 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LEIRVQGAS	256	30
2	WPLTQVTFY	105	27
3	SEDHSGSYW	231	24
4	REAGFQVKA	56	18
5	EAGFQVKAY	57	13.5
6	LGMPDPHLY	310	12
7	SEFQIPTAS	223	12
8	AEPQAGSPM	180	12
9	QELPPAPIL	166	12
10	SEPFHLIVS	68	12
11	SAARLLFSF	201	9
12	VAITVQELF	161	7.5
13	ASEDHSGSY	230	6
14	AARLLFSFY	202	6
15	DDLTDAREA	50	4.5
16	FSITVVQKA	128	3.375
17	EPFHLIVSY	69	3
18	AQMLLAASF	22	3
19	TEDNQVWKQ	244	1.8
20	CEGPFVCTEE	35	1.8



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# ANALYSIS RESULTS OF THE PROGRAM TSITES.

.....

These are the results of the analysis of the file --> LY1464-1.TXT

Beginning with residue: 1 and ending with residue: 359

AMPHI Window size: 11

A - AMPHI mid points of blocks.

R - Residues matching the Rothbard/Taylor motif.

D - Residues matching the IAd motif.

d - Residues matching the IEd motif.

SEQUENCE:  
10,518

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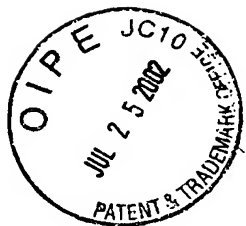
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KADSGHYHCSGIFQSP

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R.....RRRR..  
.....  
.....

155 160 165 170 175 180 185 190 195 200 205 210 215 220 225  
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DGRIVQSRGLSSEF

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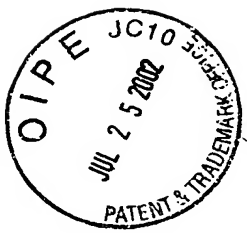
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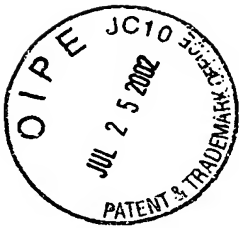




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Table 4. Immunogenic portions of Lyl464 (SEQ ID NOs 10,820-10,842)

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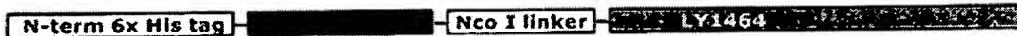
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Ra12-LY1464 profile

CORIXA CORPORATION  
Antigen Discovery**LY1464 and recombinant Ra12-LY1464**

**Researcher:** Alex Gaiger, Aijun Wang, Jonathan Clapper  
**Reference:** cloning bk813 pg150, 151, 154-157; expression bk966 pg2-3

**Description:** LY1464 is an antigen discovered by Lymphoma program. The full-length sequence was cloned through PCR amplification of normal tissue cDNA known to express the gene. The gene was cloned directly into the pCRX2 vector as an N-terminal Ra12 fusion, **Ra12-LY1464**, using restriction enzymes Nco I and Xho I, and the sequence was subsequently confirmed. The optimal protein expression conditions were determined by mini-induction screening.

**Protein Diagram of Ra12-LY1464****Cloning Strategy:**

Tumor and normal tissue derived cDNAs (from Alex Gaiger) were each used separately as templates in PCR amplification reactions with two primers (LY1464-sense and LY1464-antisense) flanking the 5' and 3' ends of the gene LY1464. As shown below, the primers contained short 5' restriction enzyme recognition sequences. The PCR products were separated on agarose gel and the DNA band of ~1080bp was gel purified. This 'insert' was digested using restriction enzymes Nco I and Xho I and ligated to pCRX2, which was linearized with the same two restriction enzymes and then dephosphorylated. The vector and insert were combined in equi-molar ratios with DNA ligase to create a completed plasmid construct pCRX2 **Ra12-LY1464**. This ligation mixture was used to transform competent *E. coli* Novablue cells. Ten individual colonies from both tumor cDNA derived and normal cDNA derived construct were picked for DNA miniprep. Miniprep samples were screened for insert through restriction enzyme digestion (Nco I, Xho I) and five positive samples were sent for DNA sequencing. Miniprep clone #4 (Corixa seq ID#90522) was confirmed and used for expression of recombinant **Ra12-LY1464** in *E. coli*.

**Cloning Primers:**

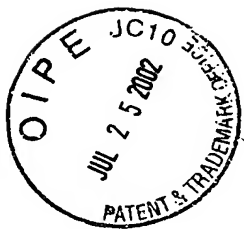
**LY1464-sense**  
5' - CGTCCATGGACatgaagctgggctgtgtcttc - 3' (SEQ ID NO: 10,843)  
prime 21bp 57%GC 56C Tm  
full length 32bp 59%GC 68C Tm

**LY1464-antisense**  
5' - CCTTCTCGAGctattcagcagtagcctttgtggtc - 3' (SEQ ID NO: 10,844)  
prime 25bp 48%GC 58C Tm  
full length 35bp 51%GC 67C Tm

**Protein Expression:**

Various *E. coli* strain/culture conditions were screened for optimal expression conditions for recombinant protein expression. Briefly, the expression construct was used to transform different expression hosts, and then mini-induction cultures were screened at varied culture temperature, culture media and/or IPTG concentration. The optimal expression condition was determined by evaluating the results of SDS-PAGE and western blot.

For **Ra12-LY1464**, The most optimal expression condition is pCRX2 **Ra12-LY1464** in Tuner (DE3) CodonPlus-RP grown in 2xYS media at 37°C induced with 1.0mM IPTG at 25°C (room temp) for 3hr.



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Ra12-LY1464 profile

CORIXA CORPORATION  
Antigen Discovery**DNA/Protein Sequence:****LY1464 (DNA) 1080bp (SEQ ID NO: 10,445)**

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**Ra12-LY1464 (DNA) 1500bp (SEQ ID NO: 10,447)**

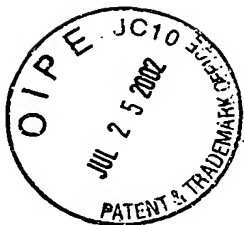
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**Ra12-LY1464 (protein) (SEQ ID NO: 10,448)**

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**Protein Info:****Ra12.LY1464**

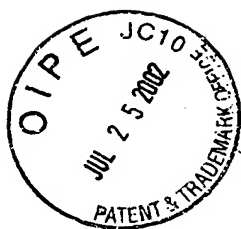
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29 Strongly Basic(+) Amino Acids (K,R)  
46 Strongly Acidic(-) Amino Acids (D,E)  
174 Hydrophobic Amino Acids (A,I,L,F,W,V)  
128 Polar Amino Acids (N,C,Q,S,T,Y)  
5.663 Isoelectric Point  
-14.119 Charge at PH 7.0



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1484  
Ly1448. DNA Sequence (SEQ ID NO: 10, 846)

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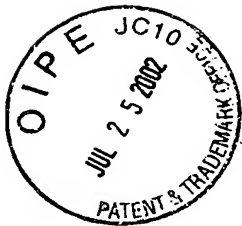
**Ly1484. Protein sequence (long)** (SEQ ID NO: 10, 847)

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**Ly1484. Protein sequence (short)** (SEQ ID NO: 10, 848)

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## a. TMpred Report for Ly1484 Long

Date:

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Black = intracellular, Red = Transmembrane, Blue = Extracellular

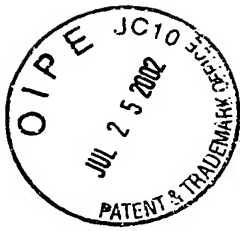
Ly1484 Long has 1269 amino acids and 5 Transmembrane Domains

Transmembrane Domain 1:	63 - 84	Score: 1.36675
Transmembrane Domain 2:	118 - 139	Score: 1.38695
Transmembrane Domain 3:	480 - 501	Score: 1.36185
Transmembrane Domain 4:	562 - 583	Score: 1.31785
Transmembrane Domain 5:	725 - 746	Score: 1.3521

## b. TMpred Report for Ly1484 (short)

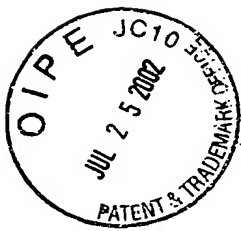
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ELDVSIALTGKPSKTS PAVTALAVSRNHTKLLVGDERGRIFCWSADG (SEQ ID NO: 10,848)

Black = intracellular, Red = Transmembrane, Blue = Extracellular



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Lyl484 has 646 amino acids and 1 Transmembrane Domains  
Transmembrane Domain 1: 102 - 123      Score: 1.3521



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Table2a: Ly1484 long MHC class I binding peptides  
(SERIDNOs: 10,849-10,908)

## HLA A2:

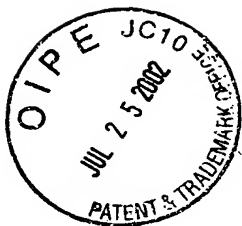
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	FLCLMHCL	145	836.3
2	YLPEFLTNC	783	818.9
3	KLYSGMPSA	57	742.3
4	FILEHIMVV	73	629.3
5	TLYSSLNKV	95	511.9
6	FLQEHMDVV	127	448
7	ILWDLHLT	1093	431.1
8	ALQGSFQV	743	403.4
9	MQYFVPPWV	654	400.9
10	ALYGHQAV	1063	222.6
11	YLVRMPPFT	730	188.5
12	CLMHCLLL	148	181.8
13	GLLSILQFL	120	130
14	VIMTFENLA	1010	118.7
15	ILAVERNKV	973	118.2
16	YLASEKKS	260	98.27
17	ELTPEFFYL	776	97.11
18	YLMYLTAA	638	84.56
19	ILLFILEHI	70	73.96
20	LLQDIALEI	563	72.72

## HLA A3

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KLMPGRQAK	292	135
2	VLLPFLWNR	981	60.75
3	CLGSYGSDK	1001	60
4	KVILYCLSK	102	54
5	CVWELSMTK	1044	30
6	LLFGHQHLY	495	30
7	PLWEETMLK	247	30
8	FLSPHEDVK	180	30
9	SLYKDHVQR	326	20
10	FLVFNDR	580	18
11	KLYSGMPSA	57	13.5
12	GLRLRQALY	1057	12
13	NLANPKIFR	672	12
14	RVWRTEDVK	1183	10
15	QVPKQLFTK	894	9
16	RMPPFTQAF	733	9
17	KLKFIQRPK	694	9
18	RIMLQKQK	622	9
19	VILQELLQK	465	9
20	IMLQKQK	623	6

## HLA A24

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	QYVFPWVL	655	300
2	FYICENFTL	502	300
3	TYNSNISFL	138	300
4	NYRRRQEL	315	264
5	DYTSETLNL	665	200
6	SYLVRMPPF	729	150
7	RYPGSDRIM	616	75
8	RPLLQDIAL	561	60
9	LYSSLNKVI	96	60
10	YTHYSSAI	717	50
11	FFPALHESL	443	36
12	NFGQVEKQL	891	28
13	SYGSDKVL	1004	25
14	GFDDFSCCL	994	24
15	EFFYLPEFL	780	24
16	YFYGDRLML	865	20
17	SFCSFQPSL	594	20
18	RGLRLQAL	1056	17.28
19	RQELYASL	319	17.28
20	KNLALSREL	1217	15.84



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CID1096 Table 2b.Lyl484 short MHC class I binding peptides  
(SEQ ID NOS: 10,901-10,968)

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	YLPEFLTNC	160	818.9
2	ILWDLHLT	470	431.1
3	ALOGGSFDV	120	403.4
4	MQYVFPFNV	31	400.9
5	ALYGHQAQV	440	222.6
6	YLVRMPPT	107	188.5
7	VLMTFENLA	387	118.7
8	ILAVERNKV	350	118.2
9	ELTPEFFYL	153	97.11
10	YLMYLNTAA	15	84.56
11	VLADYTSET	39	51.94
12	RMFHSVKST	131	45.8
13	SNFEYLYNL	11	26.76
14	KVLMTFENL	386	22.54
15	LLPPLMNRT	359	21.54
16	QLPTKPHPA	275	18.38
17	GAHLSIMNV	507	16.66
18	WDLHLTHV	472	16.5
19	FISLARKAL	198	13.51
20	CILWDLHL	469	12.25

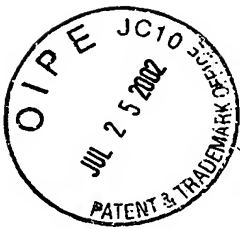
## HLA A3

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	VLLPPLMNR	358	60.75
2	CLGSYGSDX	378	60
3	CVWELSMTK	421	30
4	GLRLRQALY	434	12
5	NLANPKIPR	49	12
6	RVWKTEDVK	560	10
7	QVPKQLPTK	271	9
8	RMPPPTQAP	110	9
9	KLKFIORFK	71	9
10	TILGFVSNF	261	4.05
11	SLPGHPQPF	301	3
12	WIDLIFGYK	218	2.7
13	NLJHMIDLI	214	2.7
14	YMQYEVFPW	30	2.7
15	ELTPEFFYL	153	2.43
16	ALYGHQAQV	440	1.5
17	YLPEFLTNC	160	1.35
18	IIVASYLVR	102	1.2
19	DMTVQCHYY	87	1.2
20	QLPTKPHPA	275	1

## HLA A24

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	QYVFPFWVL	32	300
2	DYTSETLAL	42	200
3	SYLVRMPPT	106	150
4	YTHYSSAI	94	50
5	NPGQVFKQL	268	28
6	SYGSDKVLN	381	25
7	GFDDFSCCL	371	24
8	EFFYLPEFL	157	24
9	YFYGDMDL	242	20
10	RGLRLRQAL	433	17.28
11	IGLALSREL	594	15.84
12	KVLMTFENL	386	14.4
13	TFSWGFDDF	367	12
14	FYLPEFLTN	159	10.8
15	ANPKIPRDL	51	10.08
16	SFDVADRMF	125	10
17	KTSPAVTAL	614	9.6
18	KGRPRGLRL	429	9.6
19	RNKVLLPPL	355	9.6
20	EYLYLNTA	14	9

FIG. 20



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ANALYSIS RESULTS OF THE PROGRAM TSITES.

.....

These are the results of the analysis of the file --> LY1484-1.TXT  
Beginning with residue: 1 and ending with residue: 1270  
AMPHI Window size: 11

A - AMPHI mid points of blocks.  
R - Residues matching the Rothbard/Taylor motif.  
D - Residues matching the IAd motif.  
d - Residues matching the IEd motif.

(9010ND)  
19/8/97

```

5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
RDPQSEVLLSAMELPHMTSGGDAAMPFDGKEPQPSAARAAAPSLANISCTQKLVEKLYSGMFSADPRHILLFIL
.....AAAAA.....AAAAA.....AAAAA.....
RRRRR..RRRRRRR.....RRRRRRRRRRR.....
.....DDDDDD.....

80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
EHIMVVIETASSQRDTVLSTLYSSLNKVILYCLSKPOQSLSECLGLSLILGLFQEHWDVVFATYNSNISFLCLM
.....AAAAA.....AAAAA.....AAAAA.....
RRRRR..RRRRR.....RRRRR..RRRRR.....
.....DDDDDD.....DDDDDD.....

155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
HCLILLNERSYFEGFGLSPKPMSTYHQVFLSPNEOVKEKREDLPSSLSDVOHENIQKTIVOTLMQOLVAQRQOTLED
.....AAAAA.....AAAAA.....AAAAA.....
.....RRRRR.....R

230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
APKIDLSVKPGEREVKIEKVTPLNEETMLKAWOHYLAEEKSLASRSNVVHNSKVTLMWGSGLSSAMKLNPGROAK
.....AAAAA.....AAAAA.....AAAAA.....
RRR.....RRRRRRRRRRR.....RRRRR.....
.....dadd.....

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
DPECKTEDFVSCIENYRRRQQLYASLYKDHVORRKKOCHIKAAAMAWARIQEQLFGLGLWSQGSZETKPCSPWELD
.....AAAAA.....AAAAA.....AAAAA.....AAA
RRRR.....RRRRR.....RRRR.....RRRR.....

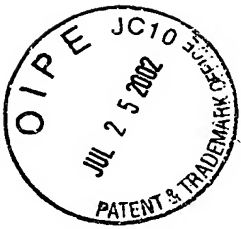
380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
WREGPARNRKRIRKLSPLEALSSGRHKBESQDNDHISQTNAEHQDELTLEAEGSPDEVGVDCQTQLTFFPALHES
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....
RRRR.....RRRRR.....RRRR.....DDDDDD.....
.....dadd.....

455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LHSEDFLELCRERQVILQELLDKEKVTQKPSLVIVQGHVSEGVLLPGHONFYICENPTLSPTGDDVYCTRKCLSN
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....
RRRR.....RRRRR.....RRRR.....RRRR.....

530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
ISDPPIFNLCSKORSTOHYSQCKMSYADMRELQARFLQOIALEIPFHNGYSKFLVPFYNDRSKAFKSFCSFOP
A.AAAAAA.....AAAAA.....RRRRRRRRRRRRR.....RRRR.....

605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
SLKGKATSEDTLMLRRYPGSDRIHLQKQKRDISHPEYLMVLTAACTCNDVMQYVPFPMVLADYTSETLNLAN
.....AAAAA.....AAA.....AAAAA.....AAAAA.....RRRRRRRRR...
RRRRR..RRRRR.....RRRRR.....RRRR.....RRRRRRRRR...
.....DDDDDD.....

680 685 690 695 700 705 710 715 720 725 730 735 740 745 750
PKIPDLSKPMGAQTKERKLFPIORFKEVEKTEGDNVQCHYTHYSSAIVASVLRMPPTQAPCALQGGSPD
AAAAA.....AAAAA.....AAAAA.....AAAAA.....A
RRRR.....RRRR.....RRRRR..RRRRR.....R
```

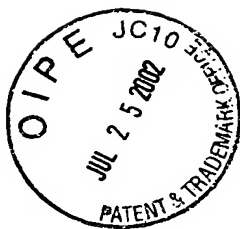


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.....DDDDDDDDDD.....  
.....ddd.....  
755 760 765 770 775 780 785 790 795 800 805 810 815 820 825  
VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGDDVQLPPWADGDPKRFISLH  
AAAAAAAAAAAA.AA.AAAA.AAAAAA.....AAAAA.....AAA.....  
RRRRRRR.....RRRRR.....RRRRR.....RRRRR.....RRRRR.....  
.....  
830 835 840 845 850 855 860 865 870 875 880 885 890 895 900  
RKALSDFVSANLHHWIDLIFGYKQGGPAAVDVNIHFPYFYGDRLSSITDPLIKSTILGFVSNFGQVPKQLF  
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....  
RRRRR.RRRR.....RRRRRRR.....RRRR.....RRRR.....RRRR.....  
.....DDDDDD.....  
.....  
905 910 915 920 925 930 935 940 945 950 955 960 965 970 975  
TKPHPARTAAGKPLPGKDVSTFVSLFGHPQFFYSLSLRPSQVTVKDMYLFSLGSES PKGAIGHIVSTEXTILA  
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....  
RRRRR.....RRRRRRR.....RRRRRRR.....RRRRRRR.....RRRRRRR.....  
DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....  
.....  
980 985 990 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050  
VERNKVLLPPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAANGRCCLCAVCPSPTTIIVTSGTSTVVCVWELSM  
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....  
RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....  
DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....  
.....  
1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125  
TKGRPRGLRLQALYGHQAQVTCLAASVTFSLVSGSQDCTCILWDLHLTHVTRLPAHREGISAITISDVSGTI  
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....  
RRRRRRR.....RRRRRRR.....RRRRRRR.....RRRRRRR.....RRRRRRR.....  
DDD.....DDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....  
ddddd dddd  
.....  
1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200  
VSCAGHLSLWVNGQPLASITTANGPEGAITCCCLMEGPANDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG  
A.....AAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....  
RR.....RRRR.....RRRRRRR.....RRRRRRR.....RRRRRRR.....  
D.....DDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....  
.....  
1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275  
EEPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTSFAVTALAVSRMHTKLLVGDERGRIFCWSADG  
.....RRRRR.....  
DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....  
.....

FIG. 21  
Page 2 of 2





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ANALYSIS RESULTS OF THE PROGRAM TSITES.

\*\*\*\*\*

These are the results of the analysis of the file --> LY1484-2.TXT  
Beginning with residue: 1 and ending with residue: 647  
AMPHI Window size: 11

A - AMPHI mid points of blocks.  
R - Residues matching the Rothbard/Taylor motif.  
D - Residues matching the IAD motif.  
d - Residues matching the IEd motif.

SEQ ID NO  
10,846

```

5  10  15  20  25  30  35  40  45  50  55  60  65  70  75
MLQKQKRDISNPEYLYLNTAAGRTCDYMOYVFPVWVLADYTSSETLNLNPKIFHDLSKPMGAQTKERKLKPI
...AAA...AAAAAAAAA...AAAAAAAAA...AAA
...RRRR...RRRRRRRR...RRRR...RRR
...ddddd...

80  85  90  95 100 105 110 115 120 125 130 135 140 145 150
GRFKEVETEGDMTVQCHYTHYSIAIVASYLVNMPPTQAPCALQGGSPDVADRMFHSVKSTWESASRENMSD
AAAAAAAAA...AAAAA...AAAAAAAAA...AA.AAAA..AA
R...RRRR.RRRRR...RRRRRRRR...
...DDDDDDDDDD...

155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
VRELTPFFYLPEPLTNCNGVEFOCMQDQTVLGDVQLPPNADGDPKPFISLHRKALESDFVSANLHNMWIDLIFGY
AAAA...AAAAA...AAA...AAAAAAAAA
RRRRR...RRRRR...RRRRR...RRRR.RRRR...RRRRRRRR
...

230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
KQGGPAAVDAVNIFKPYFYCDKMDLSSITDPLIKSTILGFVSNFGQVPKQLPTKPHPARTAAGKPLPGKDVSTPV
AAAAAAAAA...AAAAA...AAAAAAAAA...AAAA
RRRR...RRRR...RRRR...RRRR...RRRR...DDDDDD...DDDDDD...DDDDDD
...

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
SLPGHPQPPFFYSLQSLRPSQVTVKDNLYFLSGSESPKGAIGHIVSTEKTLAVERMKVLLPPLMNRTPSMGFDDP
AAAAA...AAAAA...RRRRRRRR...RRRR
D...DDDDDD...

380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
SCCLGSYGSXKVLMTFENLAANGRCICAVCPSPITIVTSGTSTVVCVMSMTKGRPRGLRLRQALYGHQAVTC
AAAAAAAAA...AAAAA...DDDDDDDDDD...DDDDDD...DDDDDD...DDDDDDDDDD
...RRRRR...

455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LAASVTFSLLVSGSQDCTCILWDLHLTHVTLPAHREGISAITISDVSQTIVSCAGAHLSLMVNVNGQPLASITT
AAAAAAAAA...AAA...AAAAA...RRRRR...RRRRR...DDDDDD...DDDDDD...DDDDDD
...

530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
ANGPEGAITCCCLMEGPANDTSQIIITGSQDGMVRVWKTEDVIMSVFGRFAGEEPLAQPPSPRGHMEKNLALSR
AAAAA...RRRRR...RRRRRRRR...DDDDDD...DDDDDD
D...DDDDDD...

605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
ELDVSIALTGKPSKTSPTALTAVSRNHTKLLVGDGRGRIPCWSADG
...RRRRR...
...DDDDDDDD...DDDDDD...ddddd

```

FIG. 22

# Ly1456P LifeSeqGold Clone Distribution

## Ly1456P LifeSeq Gold Search

LifeSeq Template	E Value of hit	Length (bp)	Libraries Found in		Clone Abundance		ORFs * (>50aa)	TMpred **
			Total #	Hemic & Immune #	Total Clone Count	Hemic & Immune		
238330_1	0	1442	55	21	78	33	294bp 177bp 252bp 198bp	No No No No

\* = Template sequence was searched for ORFs using MapDraw (4 potential ORFs identified).

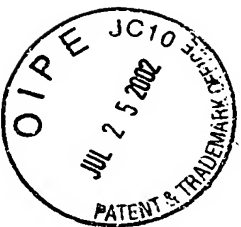
\*\* = Predicted ORFs were translated and were analyzed for potential TM regions using TMpred.

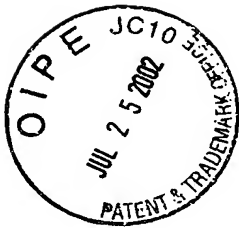
ORF#1 = 379>672 = 294bp = 98aa

ORF#2 = 555>734 = 177bp = 59aa

ORF#3 = 1037>1291 = 252bp = 84aa

ORF#4 = 1074>1274 = 198bp = 66aa



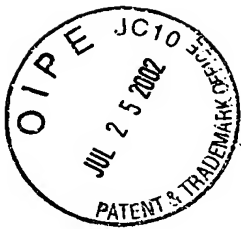


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SEQ ID NO: 10,475

```
1 gcttctcccc tgggtcttca cgtgggtcccc gctgtctgtg cgttgtgtccc tgatctcttc
61 tcttctataag gaccccaatc atattggatt agagcccatc cacaggacct aaatttttcc
121 ctttaactctt tctctgtttg ccccaagaac actcaccagc agctctttgog gctgcagcgt
181 ttaccocaaaa gtaatttggg cacaasaacat cttcccttta ttattttcac tttgtcttag
241 tgtatcaact tgggaacaaa aagacatcat tctacgtata agacatcatt ctaggttatag
301 cgttctgtct ttagtagtgg catttccatt tagaaaatat agtaattctc gatcgtgtaa
361 aatgtcaaat ccgagaaaac atagcattcc tatgtgata tttctcaaga gttgttggcc
421 aaagattcat ttgatatac ctatttttct gaaatagacg attctgatga ttgagatgat
481 tttgatgtta gttctgttta cacataactc caagaacagt ttttaattt tactttcaca
541 ttgaaataca gtcagggttg tttatgtaaa attaaatgag ctctggccaa gcacgggtggc
601 tcatgcttar aatcccagca ctttgggagg ctgagggtga cagatcactt gaggtcagga
661 gtttgacacc agcctgggca gcatggcgaa acccgtcttc taaaaaaat acatatatat
721 tagccagatg tgggtgttga tgccctgtgt cccagcttct caggaagctg aggcaggaga
781 atcatttgaa cttgaggggc agagggttga gtgagccaa atgtgtccat ggaacoccaa
841 cctgggcaac agagcaagac tctgtctcaa aaaaaaaa aaatgtctgg agtgggctgc
901 acttttttct tctctaaaca ggaataagggt taattatttc ttttaagaac cttagcaccaa
961 atacagtcac attcggagggt actgggggtt gggacttgaa catatgaatt ttgagggggc
1021 acaaggctac ccattgacaca tgtgggaacc ggtataatct ctacagagac tagaatttag
1081 atttaacagc ttgaadacag ttcaggttat tggtaacata caaaacaaaa acaattcaaa
1141 gccctttaca tcaaatat tgaaataaaa ataactattt ctacaatgta taaaagggtat
1201 gctatgttta ttagctctac ttgtagctaa tctactttta tgtttcctta cagaaaatttc
1261 ttgacatttt atgtttccgt gtaagagatt gtacagaagg caaatttttg tgttatgcaa
1321 taataatact ctaatacaaaa ttctgttatg aacttcatgt gcatatattt taatgtcat
1381 agcaattatt tttatgttgt attttcaaat aatctagatt tcatgcagca ttataaaact
1441 aactgggggt ggggacactg gctcatgctt gtaatctcaa cactttggga ggccaaaggcg
1501 ggcagactgc ttaagccacg gagtttgaga ccatcctggg caacatggca aaacccctgc
1561 tctacaaaaa atacaaaaaa aacaaaaatt agccagacat ggtgtgtcac gctgtgtctg
1621 ccagctactc aggagcttga cacaggagga tcaattgaac accggagggca gaggtctgag
1681 tgagccagga ttgtgcaact gcatctcagc tgggtgacac agcgagaccc tgrctcaaaa
1741 caaaacaaaa caaaacaaaa acaaaacaga aaacagtgtg agaagtgttc attaccacc
1801 cccccccacc cccaaagctt tccaagctcc cgacccata cagaggcaaa ggtatgcactg
1861 tgcaaaagct cctgctgggc cccaaacgct cagtcacacc caccactgoc tttgatgac
1921 tcttgacccc tccacttca atctagaccc cacacctatc ccaactatct ctcaagcaca
1981 gggggacctt gaataaagggt tttcttctctg tccctgcacc tccagacaa agagtgcact
2041 ggtttcttag acagatcaga tctgtttaa acatttaaca aggtcaagat aacttaaaat
2101 agttaccaga caaaataga tggactagta catggacagc agctaacga gacatgggat
2161 gctacgttct tttatcacac atcagatctt gacatcatat tagtaagggt gtggggcggg
2221 gacatgccat gggcagggtg gggctgcagc tggccagact gagctggccc tttctgttag
2281 ttgaaccttg gggatattga ggcgtgtgc aatgggtgcca cctgatgga ctttgtagaa
2341 taacctctct cctagtttt cttcatcttt aagttcctaa agagagactg aaatttcaa
2401 tctggtttct tgttgcctat tattgtcaaa tgaaaagtgc aaactgtgtt acccactct
2461 cttgattttt atctgctcaa aaatgaaat ctcagctata ttcactgata tattatggaa
2521 agaacactgg acttaaggga tttgggttca gatccactt tgggcaact actagtata
2581 ggtatttgga aagttactca acatctgcat gccatttta tgatctggag aatggaaata
2641 ataggattct tgtgaggatt accggagggt atatatgac atctgcgtcc ataaatcaag
2701 cctgggtgtt gggagggtgt gcgtcaccat catgcatctt ctgaaggagg ctgaccagc
2761 tctaccttta atggctggga tttacttgtc ttttgggtcc tttccacctg tttgccagca
2821 gaggctaaag tttgtgtgga ggcactctct cagcagatga gttgagacca tcttggtcaa
2881 catggtcagg accaccttgg ggcctctgtg cagggcagtg cccacctga tgcctacgt
2941 ggtcagattg agagcataga catggggcca tgacctccat aaacccccac ccagtgtcac
3001 atggcagccc aaggaaacct cttagccctg ggttcttctg ctgtaaaac aggttaacgt
3061 aacaagggga gctacttagt aaaccaaaaa aaaaaaaact aaactacaat tctgttctg
3121 ggtatttttg ttttgtttg ttttggagt ttatttggct gctgttttac tctatttcc
3181 cagagacaaa tgaagcgtaa gaggtgttct ttgcatfact ataaaggaat acctgagact
3241 gggtaartta taagaaaaga gaagtctttt tgttttgggt ttgttttgag acagagtctt
3301 actcttattg cccaggctgg agtgcaatgg actcacttga actcctgcat accctgccc
3361 cccagggtta agcaattctc ctgectcagc ctcctgagta gctgggatta caggcatggg
3421 ccaccatgac cggctaattt cgtattttta gttagagacag agtttctcca tgttggctg
3481 actggtctca aactcccaac ctgaggggat ccgcttgcct tggcctccca aagtgtctgg
3541 attacgggca tgagccacog tgcctggcta gaaaaggagt ttaattggct cacagtcttc
3601 caggctgtaa ggaagcatgg ccccaacatc tgctcatctt ctgaggaggc ctcaaggagc
3661 ttatgatcat ggcagaaagg gaagggggag caggcaogcc acatggcaaa agcaggaaca
3721 agagagacag ctggtgttgg ggggtgccac agactcttca atgaccaggt ctcaagaa
3781 ttcactcact atgatcagga cagcaaccaag ccatgaggga tgggtccca tgatcccaac
3841 acctcccacc agatcccacc tccatcactg gggatcacaa tgcaacctga gatttgggag
3901 aggacaaaaa tccaaactat atcaagcatc ttcttcccc tttctccctt cccctcctga
3961 tcttggggag aagaggctgc tgtgtgttct tgaagggtg agtgttctca cccaccccca
4021 acccccaag taagaaactc ttatgtttca ggcctcagg gttgtgggag aggtgttccc
4081 agaggagcag ggcgtgagct tggcagcttt agttgaagag gctgggatag ataggggggc
4141 aggggtgtgt gttctcagaa atgggtgagga gtagggggga aggggtgtcc aggtgtctc
4201 ggggtgtgag catgaatacc cagaggctga gcttcaactc atcagcaactg ctccgggga
4261 ccacagtgac tgaagagtga acctctgagc agtgtcagg gctgtctgag gcccggaag
4321 ccagttctct gaattgttga agacctgtc aggtccacag gaacccagaa gccaggaagc
4381 acaacaaatt ggtttctcgc ccacgtgag tagatggag ctagaaaacc aaagaaagcc
4441 aggtgtgttg gctcaogcct gtaatccag cacttcggga gggcgaggag ggcggtcac
4501 ttgaagtcag cactttgaga ccagcctggc caacatgggt ccaactact tgggtgtctg
4561 atacaaaaat tagctgggca tgggtggcat cacctgtaat cccactact tgggtgtctg
4621 aggcagtaga atctctgaa ctgggaggca gagattgagc tagactgaga tggaccact
4681 gcactccagc ctgggcgaca gagtggagct ctgtcttaca aaaaaaaa aagaaaaag
4741 aaacaaagaa acaaaagaaa agaaaatcaa tggcccttgc gccagagtgt ctggaggga
4801 gtccacactg acacgccac ggggggagct gctgaaagca tccccagtc cagtgtgccc
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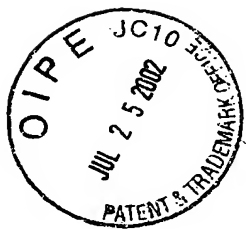
FIG. 24  
Page 1 of 11



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4861 cegtgagcac cgeccacctgt tccccgcttt cctggccacc gtacatacat ttgttcatgt  
4921 ttatagactc tgaatataga gacccacac aagaagagaa aggtcagaa aaacaatgtt  
4981 atgacctgct tcctgaggca ccttgccctgc aggaagtgtt ttccacagca agaaattctg  
5041 actccaggac ccatattttt agcaggaaca tggtcagtca acacacatcc tctaggcctg  
5101 ccttggaacca gatgaccagg aggaagcagc cgtgagtcac agggagaaag cgggtggctc  
5161 tgacagggac gcctgctgct cgcgaggga acagctttcc cctggtttca gtttagaagg  
5221 tcaggggacg cctgaccaca caaggctcac gggaaactgt gaggcgggcc cctcaggcca  
5281 caatcagcag gtgcccacca tggcttctct cctggcaggt gaggacttca gtttttctcc  
5341 atggcttggc tcacctgttc tcttattctc agagccataa tcacctctc cctgccccag  
5401 cctggagctc tctgagaccc tccactatag taaccagcac agcctagaga gggtaaatcc  
5461 tccggtgccc ccaacatccc accttcatgt tgcagcgagg cccaaaatgt cccagaagaa  
5521 aaacaaactc catcgcacac caaaaaccca ccaaaaacg tgaatcacc ttcataattt  
5581 ggggaagtata aacatagttc tatttgttct gtaacgtatt ttcatgatc aggaaatgaa  
5641 gacaaaagaaa ggctttggga attgttttat ggagaggaca ccatcttcca ggtccttgcca  
5701 cctcagggct cccatcttcc agcccttcca gagctgagcc cggaggggctg gggccgccc  
5761 ctccctgctc ctgagccaca gaagcccaag gctggccctg aagacctaac agcctcaggc  
5821 atttgagccc cccttggcct aaaaaggctg ttaagagagg tgcagacgtg ggccttggcc  
5881 attcaccctc agaggaggct gcgacttcca ccccgacaag agtaccctta ggactgtgga  
5941 gtgcagagga cagcgaccgt tgactaggta cctggtgcag ggtcctggcc tccctccctg  
6001 tagcccgata tgggaaggga cacagtccaa gtccatgttc atgtgtctcc tccaggaggc  
6061 ctteccaaac atcttctcga tgcagagtaa ctcacagatc ccatatagaa atagacctg  
6121 gaagggatct ctcttcttgc aaatgaagaa actgaagacc agagatgtac ctcaaatcac  
6181 acagcagata accggcagag ccaggaggct cctctgcccc caggccagag agggcttgca  
6241 atctggcttc cgagcagtggt ttcccaactc cggggccatt acaatcacc tggatcccc  
6301 ccagtggaat gactctctgg ggggtggtgct tgaaggctg gtggtggtga aggtccctc  
6361 ggtgattctc atgcagccag attggagaac cctttagatt caggcatgga ggttccacct  
6421 ggttccagat cacatggcca tttggtctca agaaagtac agccctcctg agtctcactg  
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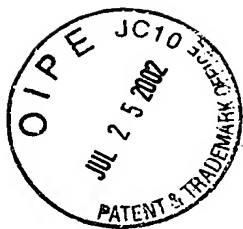
FIG. 24  
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FIG. 24

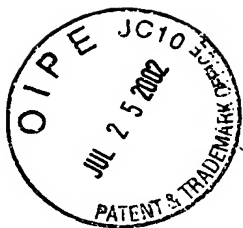


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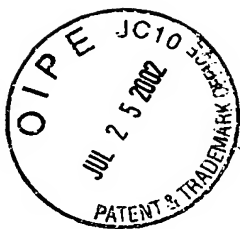
FIG. 24





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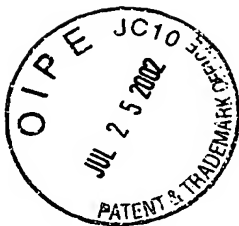


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FIG. 24

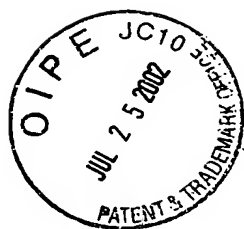




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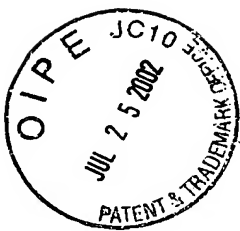
FIG. 24  
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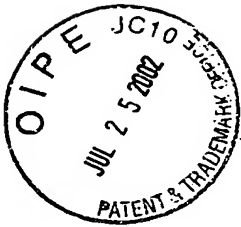
FIG. 24



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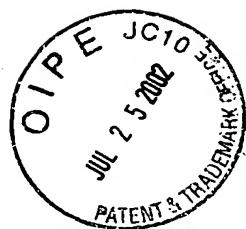
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FIG. 24  
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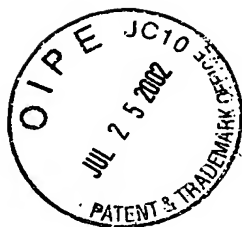
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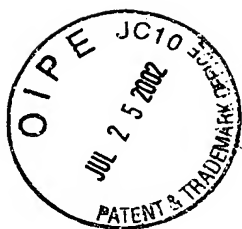
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FIG. 25

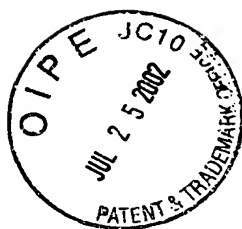


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gatagagaaa	ggagttcatg	aaggcagaaa	tgccctgggg	ccacgaacat	cccagtggtg	2880
ccctggacgg	gacatcatgc	tgggcaaac	agctaaaaat	cgggtgaaga	ccagatttct	2940
tgacacatgg	ggtgacggga	tgctccctag	agagcttcaa	gtggattctt	tgctttttat	3000
tttctctctt	aataaaaaat	tatgatgttt	acattgtcag	agaaaaaaa	aaaaaaaaaa	3060
ctcgtagggg	gggcccgtac	ccaatcgctt	gtgatgatgg	tatac		3105

FIG. 26



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## Lyl488 Protein Sequence (SERID NO: 10,961)

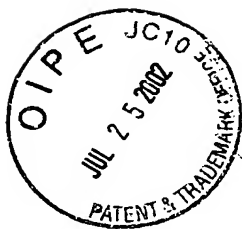
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ALEEHFRDDDDGPVSSQGYMPYLNKYILDKVEEGAFVKEHFDLCWTLTAKKNYRADS  
NGNSMLSNQDAFRLWCLFNFLSEDKYPLIMVPDEGDEGNHPSPEVPSTKHPNKTODP  
PESPKQSVPKSCWGRLEWEPDRALPGVGAGNTTCCSYQAFLLLLQVEYLLKKVLSSMSL  
EVSILGELEBLLAQEAQVAQTGGGLSVWQPLELPNSGRCLRGVGRDTLSMAIHEVYQEL  
IQDVLKQGYLWKRGHLRRNWAERWFQLOPSCLCYFGSEBCKEKGIIPLDAHCCVEVL  
PDRDGKRCMFCVKTANRTYEMSASDTRQRQEWTAIQAIRLQAEKTSLHKDLKQKR  
REQREQRERRRAAKEEELLRLQOLOEESKERKLOEELLQEAQRAERLLQEEERRRS  
QHRELOQALEGOLREAEQARASMOAEMELKEEBAARQORIKELBEMQORLQEAQLE  
VKARRDEESVRIAQTRLLEEEEEKLKQLMQLKEEQERYIBRAQOEKEELQEMAQQR  
SLQQAQQLEEVQRNRQRADEDVEAAQRKLQASTNVKHNWVQMNRLMHPIEPGDKRP  
VTSSSFSGFQPPLLAHRDSSLKRLTRWGSQGNRTSPSNSNEQOKSLNGGDEAPAPAST  
PQEDKLDPAPEP"

## Lyl488 DNA Sequence (mRNA) (SERID NO: 10,970)

1 gaactgctca agtccatctg gtacgccttt accgcgctgg acgtggagaa gaggtagaaa  
61 gtctccaaagt cccagctcaa ggtgctgtcc cacaacctgt acacgggtcct gcacatcccc  
121 catgaccctcg tggccctgga ggaacacttc cgagatgatg atgacggccc tgtgtccagc  
181 cagggataca tgccttacct caacaagtac atcctggaca aggtggagga gggggctttt  
241 gttaaagagc actttgatga gctgtgctgg acgctgacgg ccaagaagaa ctatcgggca  
301 gatagcaacg ggaacagtat gctctccaat caggatgcct tccgcctctg gtgcctcttc  
361 aacttcctgt ctgaggacaa gtacctctg atcatggttc ctgatgaggg tgaagaagg  
421 aaccaccgga gccctgaacc agtgcctctt actaaacacc caaacaagac ccaggatccc  
481 ccagaaagtc ctaaacagag tgtcccaaaa agctgctggg gcaggctctg ggagccagat  
541 agagcactcc ctggtgttgg tgcctggcaac accacctgct gcagctacca ggcttccct  
601 ctctgtctcc aggtggaata cctgctgaaa aaggtaacta gcagcatgag cttggagggtg  
661 agcttgggtg agctggagga gcttctggcc caggaggccc aggtggccca gaccaccggg  
721 gggctcagcg tctggcagtt cctggagctc ttcaattcgg gccgctgcct gccggggcgtg  
781 ggcggggaca cctcagcat ggccatccac gagggtctac aggagctcat ccaagatgtc  
841 ctgaagcagg gctacctgtg gaagcgaggg cacctgagaa ggaactgggc cgaacgctgg  
901 ttccagctgc agcccagctg cctctgtctt tttgggagtg aagagtgcaa agagaaaaag  
961 ggcatatccc cgtggatgc acactgtctg gtggaggtgc tgcagaccg cgacggaaag  
1021 cgtgcatgt tctgtgtgaa gacagccaac cgcacgtatg agatgagcgc ctgagacacg  
1081 cgccagcgcc aggagtgagc agctgccatc cagatggcga tccggctgca ggcggagggg  
1141 aagacgtccc tacacaagga cctgaagcag aaacggcgcg agcagcgga gacgaggag  
1201 cggcgccggg cggccaagga agaggagctg ctgcggtgca agcagctgca ggaggagaag  
1261 gagcggaagc tgcaggagct ggaagctgctg caggaggcgc agcggcagc cgagcggtg  
1321 ctgcaggagg aggaggaacg gcgcccagc cagcaccgag agctgcagca ggcgctcag  
1381 ggccaactgc gcgaggcgga gcaggccggc gcctccatgc aggtgagat gtagctgaag  
1441 gaggaggagg ctgcccggca gcggcagcgc atcaaggagc tggaggagat gcagcagcgg  
1501 ttgcaggagg ccttgcact agagggtgaa gctcggcgag atgaagaatc tgtgcgaatc  
1561 gctcagacca gactgctgga agaggaggaa gagaagctga agcagttgat gcagctgaag  
1621 gaggagcagg agcgctacat cgaacgggag cagcaggaga aggaagagct gcagcaggag  
1681 atggcacagc agagccgctc cctgcagcag gccagcagc agctggagga ggtgcccag  
1741 aaccggcaga gggctgacga ggatgtggag gctgccaga gaaaactgcg ccaggccagc  
1801 accaactgta aacactggaa tgtccagatg aaccggctga tgcacaaat tgaacctgga  
1861 gataagcgtc cggtcaccag cagctccttc tcaggcttcc agccccctct gcttgcctac  
1921 cgtgactcct ccctaaagcg cctgacccgc tggggatccc agggcaacag gacccctcg  
1981 cccaacagca atgagcagca gaagtccctc aatgggtggg atgaggctcc tccccggct  
2041 tccaccctc aggaagataa actggatcca gcaccagaaa attagcctct cttagccct  
2101 tgttcttccc aatgtcatat ccaccaggac ctggccacag ctggcctgtg ggtgatccca  
2161 gctcttacta ggagagggag ctgaggtcct ggtgccagg gcccaggccc tccaaccata  
2221 aacagtccag gatggaacct ggttcacctc tcataccagc tccaagcccc agaccatggg  
2281 agctgtctgg gatgttatc cttgagaact tggccctgtg ctttagaccc aaggaccgga  
2341 ttcttgggct aggaaagaga gaacaagcaa gccggggcta cctgccccca ggtggccacc  
2401 aagttgtgga agcacatttc taaataaaaa ctgctcttag aatgaa

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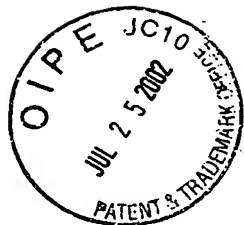
46/52

# TMpred Report for Ly1488 (SEQUENCE: 10,969)

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DSNGNSMLSNQDAFRLWCLFNFLSEDKYPLIMVPDEGDEGNHPSPEPVPS  
TKHPNKTQDPPESPQSVPKSCWGRLEWEPDRALPGVGAGNTTCCSYQAPL  
LLLQVEYLLKKVLSSMSLEVSLGELEBLLAQEAQVAQTTGGLSVWQFLEL  
FNSGRCLRGVGRDTLSMAIHEVYQELIQDVLKQGYLWKRGLRRNWAERW  
FQLQPSCLCYFGSSECKEKKGIPLDAHCCVEVLPDRDGGKRCMPCVKTAN  
RTYEMSASDTRQRQEWTAAIQMAIRLQAEKGKTSLEKDLKQKRREQREORE  
RRRAAKEEELLRLQQLQEEKERKLQELLELLQEAQRQAEELLQEEERRRS  
QHRELQQALEGQLREAEQARASMQAEMELKEEEAARQRRIKELEEMQQR  
LQEAQLQLEVKARRDEESVRIAQTRLLEEEEEKLQMLQKKEEQERYIERA  
QQEKEELQQEMAQQSRSLQQAQQQLBEVRQNRQRADEDVEAAQRKLQAS  
TNVKHWNVQMNRLMHPIEPGDKRPVTSSSFSGFPPLAHRDSSLKRLTR  
WGSQGNRTSPNSNEQQKSLNGGDEAPAPASTPQEDKLDPAPEH

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1488Rp3-329A5Chr6 has 756 amino acids and 1 Transmembrane Domains  
Transmembrane Domain 1: 199 - 220 Score: 1.3061

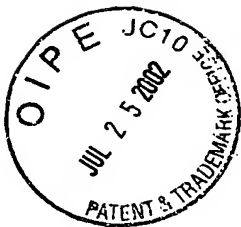


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Lyl449 and Lyl480 matches Lung cancer associated  
polynucleotide sequence SEQ ID 10,476

cttaaagagg	taatttagcc	atcattctta	tgccagcaga	tataaataaa	cttggaccca	60
tctgggtcttc	agctaaacct	gagacatttt	aaagtgcattg	gacagccatg	gacagcaggc	120
cctcctctaa	caggggatgc	aaggcatgga	gaaagacaat	cagtacccaa	gctcagccac	180
agaagacagg	agtcactcat	ataactctgt	tttagaagtt	tttggtagcc	acgcacactt	240
tctgaaatca	cactatctgg	tggtttaatc	atatttttaa	agacagaatc	cctgagtgct	300
gagcagatcc	tcaaaacaca	tttagaatcc	ctgaaattag	aaagatcaat	gacaaaaatat	360
ctgtcagcca	ggccacaaac	agggtgtaaaa	ttatgaaagg	agtgggtgga	tgtgccaagt	420
ttggtaaagt	ggtgactgca	tctgagaaag	aggctgtgag	gctgaaactct	tgggtggcttc	480
cttcgtaac	ttccagaggg	agctttcaac	acaggccccg	tgtctgtagg	aatacggtag	540
caactatgta	ggaagtgcgt	ggagttttct	gtcttctttc	tgtgtgattt	ttggcctttt	600
tatcagcact	tctccccctcc	cagagcctcg	gggatgccaa	acatccagaa	tgtgatggga	660
caagatgggg	gcaggggcct	caactccctg	cagaggtccg	gccaggtctc	cttgtccctg	720
gacaatctcc	tgagcctctc	tgcttggtgg	agcaggcacc	tgtgtgcaga	attcccactg	780
tggccagcac	gaggaagtct	tttctagtga	aaatgtgtct	tgtggtcagg	aataattatc	840
ctttccccctg	tagccaccaa	ggagggcaaa	tagagaaagg	taacctaat	gaaggattgg	900
tcatgtgaaa	agggctacat	ttgggaagct	gggaaaggcc	tccaggcttc	tagagcagct	960
agcttgggct	ggattctcay	accagagctg	ccccttggat	tgttctaccc	aagcttttcc	1020
ctgggggtctg	ggctcactcc	ataaggtaag	gtgcctttta	ccttatggtc	cttcttttagc	1080
aggtaacaaa	ggagcatcag	gggcaggctg	ccctgggtggc	atcacactgg	ctagtggaggc	1140
cgtgaatatc	ttgtccccc	gcagggccga	cagtttctat	cacagaaaac	agtgtgttca	1200
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tgcaagtccg	cctggatttt	cacttgacga	ggctacagct	gcattgtcag	gtctcccagc	1380
cctgcagaga	gctccctcca	ctggtttagca	gtgtgtgtgt	ttttccattc	atttcagaag	1440
agctacattg	tgtcactgga	cattttttaa	aactgtgatt	tttaataaaa	atttaaaatt	1500
tgaaaaaaa	aaaaaaaac	ctcgggggca	acttttrggg	gggccggggc	ccwtgcggtt	1560
t						1561

FIG. 29

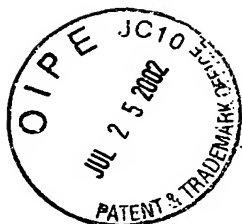


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Homo sapiens chromosome 17, clone RP11-956N15, complete sequence (bp1-10 000)

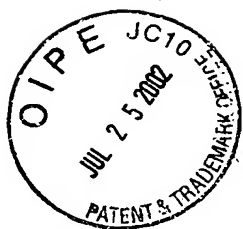
(SEQ ID NO: 10,474)

1. t g t a t g t a t g t g t g t g t g t g t a a g g t g t a t g t g t g t a t g t g t a t a t g t  
61 g t a c t g c g t g g t g c a t g c a t g t t c t g t g t a t t g t g t g c a t g t g t a t g t a t g t g t g c c c g  
121 t c t c t g c a t a t g t g t a t g t a t a t g t g t a t g t g g g t a c a g g t g t a t g t a c a t g c a t g c a  
181 c a t g t g t g c a c a t g t g t g a a t g c a t g t g t a c a t t t g t g c a t g t c t t a t g t g t g g a t g  
241 c a t g t g t t c a t g t a a a t g c a t g c a t t t g t g c c c a t g c a c a t g t g t a t g t a c a t g t g t g c a  
301 t a t a c a t g t a t g c a c t g a c a t a t a t g c a t g t g c a t a t g t a c a c g t g t g c a t g c c t t c t  
361 g t g c a t g t g t g a a t g c a t g t g t g c a t g t g g a t g t a t a t g t g t g c a t g t c t g c g c a t g t g t  
421 g t a a c c t c c t t a g a a c a g g c a g a a a t t g g g g c t c t g g a a t c c t t t c t t t g c c t a c c g c a g  
481 t t c c t t t t a g g c t g c t t c a t a g a g a a g g g a t a g c t c a a a a c c c a c a g c c t g c t t t g g  
541 c c t g a t g g g g g a t t t t c t g g g t c t c c t c a g t c t g t c t t t a t a g g c a g g c a t g g g c t g t  
601 c a g g c c c t g g c t g g g t a g a t g c t c t g c t c a t g a a t a a a g a t a g a g g c a g g g c a g g a c a g  
661 g g c c c t c c c t g a t g g g c c t c c c g c g t t c t g t g t g t g g a a t c t c a c a g t c a a c t t t g a  
721 c c t g t g c a c a t c c a c t t t t t t t t t g a g a t a g g a t c t t g c t c t g t c a c c c a g c t g g g a g t  
781 g c a g t g g t g c c a t c a c a g e t c a t t c a g c c t c g a c c t c c c a g g t c a a g c a a t c a t c t t c t g  
841 c c c c a g c c t c c a a g t a g c t g g g a c t a c a g g t g c a t a c c a c c a c c c g g c t a a t g t t t t  
901 g a t t t c t g c a g a g c t a a a g t c t t a c t a t g t g t c c a g g c t g g t c t c a a a c t c t g g g c t c a  
961 a g a g a t c c t c c t g c c c t t g g g c t c c c a a a c t g c t g g g a t t a c a g g c a t g a g c a c t g c a c c  
1021 c g g c a a c a c a t t c a c t t t t t t g g g a c a t g g c a g g a c t t a a t g t t t t a g a a a c a t t t a  
1081 g c t a c c c c t t t g a c a a t g c t g t t g a c a c t a t t g a c a g t g t g a c t t a c c a c a c t a a t  
1141 a a c t t c c a t g a a a a t c a t c a c a a g c a a a t t t a a a t t t t t a t t a a a a t c a c a g t t t t t  
1201 a a a a a t g t c c a g t g a c a c a a t g t a g c t c t t c t g a a a t g a a t g g a a a a c a a c a c a c t g c  
1261 t a a c c a g t g g a g g g a g c t c t c t g a g g g c t c g a g a c c t g a c a a t g c a g c t g a g c c t t  
1321 g c a a g t g a a a a t c c a g g c c g a c t t g c a g t c a t t g g a c t g a t g t c c a a g t g c a a t c a c c a t  
1381 a c a g c a g c t a c a g g c a g g g c t g g t g a t a g g a g t a t g g g a g a g g a c a c g c t c a g a t g a  
1441 a a a c a t g c a t g c a a c g a t t t t c a c c a c t g a a c a c a c t g t t t c t g t g a t a g a a c t g t c g  
1501 g c c c t g c t g g g g a c a a g a t a t t c a c g g c t c a c t a g c c a g t g t g a t g c c a c a g g c a g  
1561 c e t g c c c c t g a t g c t c c t t t g t t a c c t g c t a a g a a g g a c c a a a g g t a a a a g g c a c c t  
1621 a c c t a t g t g a g t g a g c c c a g a c c c c a g g g a a a g c t t g g g t a g a a c a a t c a a g g g c a g  
1681 c e t g g g t a t g a g a a t c c a g c c a a g c t a g c t g c t c t a g a a g c c t g g a g g c c t t c c c a g  
1741 t t c c c a a a t g t a g c c c t t t c a c a t g a c c a a t c c t t c a a t t a g g t a c c t t t c t a t t t  
1801 g c c c t c c t t g t g g t a c a g g g a a a g g a t a a t t a t t c c t g a c c a c a a g a c a c a t t t t c a  
1861 c t a g a a a a g a c t t c c t g t g c t g g c c a c a g t g g g a a t t c t g c a c a c a g g t g c c t g c t c c a  
1921 c c a a g c a g a g a g g c t c a g g a t t g c c a g g a c a a g g a g a c c t g g c c g a c c t c t g c a g  
1981 g g a g t g t g a g c c c c t g c c c c c a t c t t g t c c c a t c a c a t t c t g g a t g t t g g a t c c c a g  
2041 g c t c c t g g g a g g g a g a a g t g a t a a a a g g c c a a a a t c a c a c a g a a a g a a g a c a g a  
2101 a a a c t c c a c g c a c t c c t a c a t a g t g c t a c c g t a t t c c t a c g a g c a c g g g c c t g t g t  
2161 g a a g a c t c c c t c t g g a a g t t a c a g a a g g a a g c c a c c a a g a g t t c a g c c t c t c a g c c t c t  
2221 t c t a g a t g c a g t c a c c a c t t a c c a a a a c t t g g c a c a t c c a a c c a c t c c t t t c a t a a t t t  
2281 t a c a c c t g t t t g t g g c c t g g c t g a c a g a t a t t t t g t c a t t g a t c t t t c a t t c a g g g a  
2341 t c t c a a a t g t g t t t g a g a a t c t g c t c a g c a c t c a g g g a t c c t g t c t t a a a a t a t g a t  
2401 t a a c c a c c a g a t a g t g t g a t t t c a g a a a g t g t g c t g g c t a c c a a a a c t t c t a a a c a c  
2461 a a g t t a t a t g a g t g a c t c c t g t c t t c t g t g t g c t g a g c t t g g g t a c t g a t t g t c t t t c c c  
2521 a t g c c t t g c a t c c c t g t t a g a g g a g g g c t g c t g t c c a t g g c t g t c c a t a t t t a a a  
2581 a t g t c t c a g g t t a g c t g a a g a c c a g a t g g g t c c a a g t t t a t t a t a t c t g c t g g c a t a a  
2641 g a a t g a t g g c t a a a t t a c c t c t t a a g t t g t t t t t t t g t t g t t t g t t t g a c a g a g t c t  
2701 c g c t g t g a t g c c a a g c t g g a g t g c a g t g g c a t g a t c t t g c t c a c t g c g a c c t c c g t t t  
2761 c c t g g g t t c a a g c g a t t c t c t g c c t c a g c c t c c c a g a t a g c t g g g a c t a c a g a c a c a t g  
2821 c c a c c a t g c c c g g c t a a t t t t g t a t t t t t a g t a g a t g g g g t t t t a c c a t a t t g g c c a  
2881 g g c t a g t c t c a a a c t c c t t a c c t a a g t g a t c c a c c g c c t c g g c t c c t a a g t g c t g a  
2941 g a t g t c t c t t t a a c t t t c a a g a g g t a c a g c a a a c t g a a t c a a t g g g t g a t g a c t t c t t  
3001 a a a g a t c a a a c a t g a a g a t g a g g a t t a g t t a a g a c c a g a a a a t c a t t c t c o g a t c t t g a  
3061 t c t t c a a c t c a a a t t c a c a c t c c a a a a g g c c t g t t t g t g g t a g a g c t c a g g g t c t t g g c  
3121 t g t t c t g a a t t a a c t t t c t t t g g a a a c t c t t t a g a t g c t t t g a t c c c t g t g t g c c  
3181 c c c c a t t g c a g a c a c a g a a a g c a c a g g g g a t c t t g g c g g c a c c c t c t c t g t g g a g a g a  
3241 g g a a g g t g t g g a c c a c g t t c a g a g g a a g g c a g c c t g a a g c t g c c t c a g t g a g a t g c t g g  
3301 g g g a t g g g c c t c t t g c c c c t g c t g t g c a g c c c c a t g c a g g g t t a t t t a c c a g t c a c c  
3361 a g g t c t t c a a g a c a g t c t g c a g g a g a g a g g a t t t c a g g g g a a a g t a a g c c a a g c c a a t t  
3421 c a t t c t c a t g g t c c c c t t t t a t c a a a c a t g t a a g t c t t c c a t c t c a t a c a g a g a c a g  
3481 c a a a g c a g t a t c c a g g c c t t t t t t t t t t c t t t c t t t c t t c c t t a a c t g g c t a c a t g  
3541 c t t a g a a a c t g c a c t g g t c a a a c t t g a t t t c t t t t t t a a g c c t c a a a a c a t t t t t a t t g  
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3661 t c t g c c t t t g c c t c c c t t c a g g a t c a c a t g c t a a g g c a t c c t t g g g c a t t t g g a a a a g  
3721 g c g c t t g g g g t g a g a g t g c t c t a g g c c a c t c t g c a a t g t c c c t g g g c c c g a t g a g t a a c  
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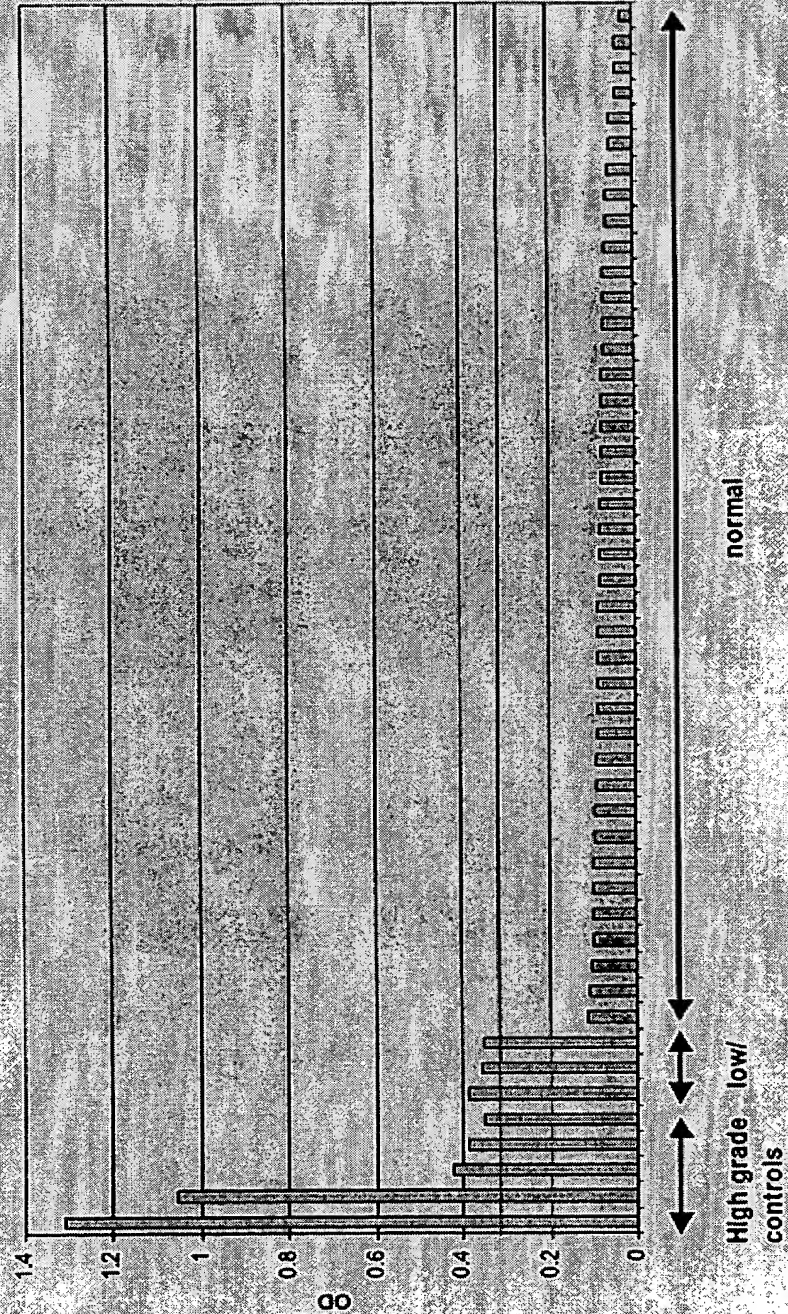
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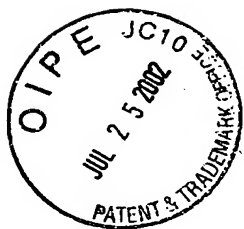
**Detection of Ly 1448P specific serum antibodies in  
lymphoma patients**



**FIG. 31**







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# Detection of TCL-1 specific serum antibodies in lymphoma patients

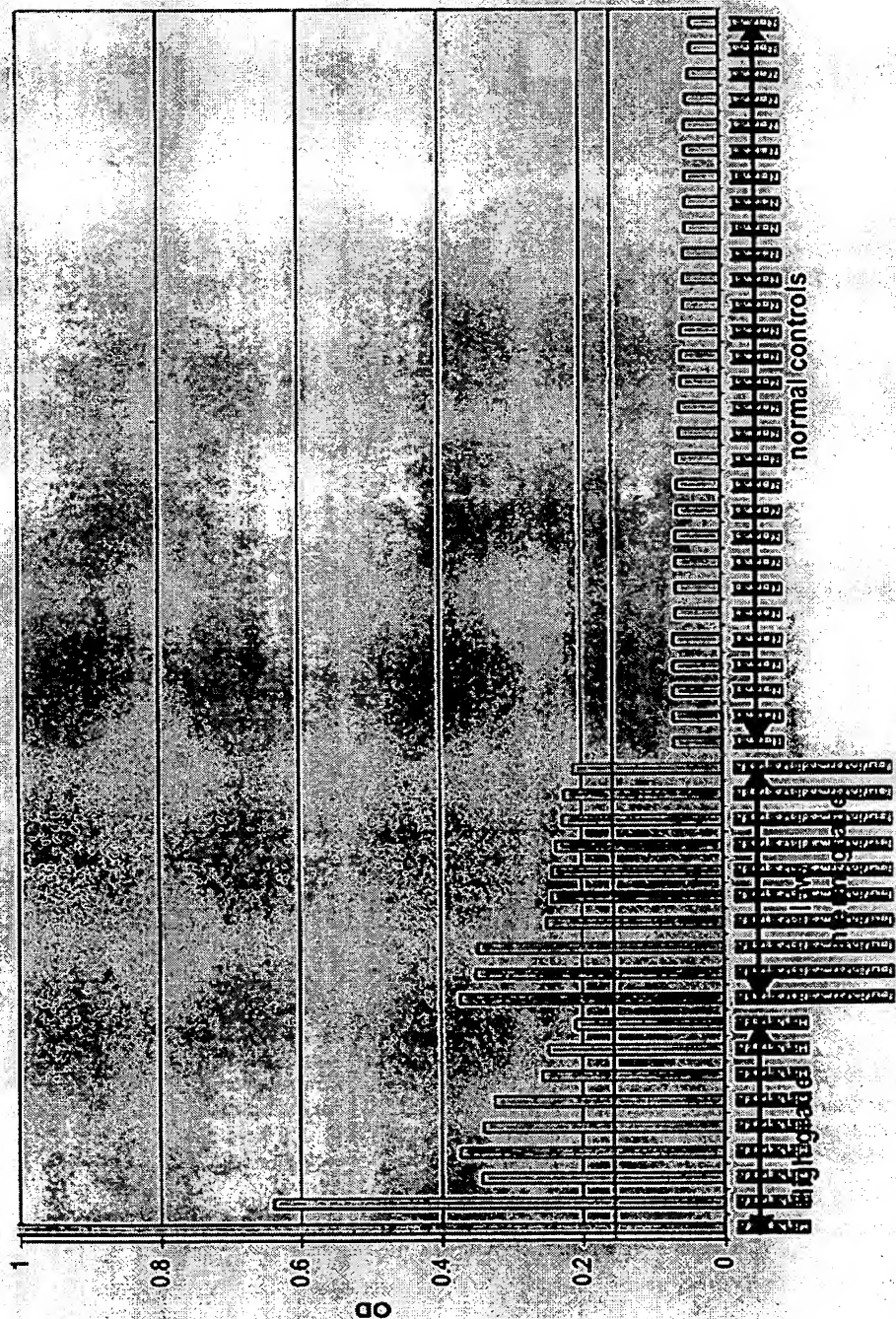


FIG. 32